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OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 02:08:08 ; Search time 520 Seconds
(without alignments)

14173.227 Million cell updates/sec

Title: US-09-715-876-7_COPY_52_1296

Perfect score: 1245

Sequence: 1 aagacaatcactgggtgtttt.....cagtggtggtacagtcca 1245

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1245	100.0	3786	10 AAD62305	Aad62305 Candida a
2	1046.6	84.1	3813	10 AAD62309	Aad62309 Candida a
3	949	76.2	4383	10 AAD62312	Aad62312 Candida a
4	947.4	76.1	3360	10 AAD62307	Aad62307 Candida a
5	895	71.9	1404	10 AAD62306	Aad62306 Candida a
6	733.4	58.9	1407	10 AAD62308	Aad62308 Candida a
7	713.8	57.3	1404	10 AAD62313	Aad62313 Candida a
8	574.6	46.2	4332	10 AAD62310	Aad62310 Candida a
9	393.6	31.6	6897	10 AAD62311	Aad62311 Candida a
C 10	82.4	6.6	100	2 AAG62588	Aag62588 Candida a
C 11	82.4	6.6	100	2 AAG62590	Aag62590 Candida a
C 12	76	6.1	100	2 AAG62589	Aag62589 Candida a
C 13	68	5.5	100	2 AAG62592	Aag62592 Candida a
14	61.4	4.9	5511	3 AAB61847	Aab61847 Cryptospor
15	61.4	4.9	5511	6 ABT04776	Abt04776 C parvum
16	61.4	4.9	7334	3 AAG61846	Aag61846 Cryptospor
17	61.4	4.9	7334	6 ABT04775	Abt04775 C parvum
C 18	57.2	4.6	100	2 AAG62593	Aag62593 Candida a
C 19	57	4.6	100	2 AAG62591	Aag62591 Candida a
C 20	56.4	4.5	204803	12 ADQ97348	Adq97348 Mouse can

21	55.4	4.4	436	4	AAI12933	Aai12933 Probe #28
22	55.4	4.4	436	4	ABA54635	Aba54635 Human foe
23	55.4	4.4	436	4	AAI34296	Aai34296 Probe #29
24	55.4	4.4	436	4	ABA44186	Aba44186 Human bre
25	55.4	4.4	436	4	ABA24419	Aba24419 Probe #28
26	55.4	4.4	436	4	AAK28369	Aak28369 Human bon
27	55.4	4.4	436	4	AAK02925	Aak02925 Human bra
28	55.4	4.4	436	4	ABS27968	Abse27968 Human liv
29	55.4	4.4	436	5	AAI02854	Aai02854 Probe #28
30	55.4	4.4	436	6	ABS02878	Abso2878 Human gen
31	55.2	4.4	5163	2	AAV20700	Aav20700 Cryptospor
32	55.2	4.4	5163	3	AAA61849	Aaa61849 ORF encod
33	55.2	4.4	5163	6	ABT04778	Abt04778 C parvum
34	55.2	4.4	5318	6	AAA61848	Aaa61848 DNA encod
35	55.2	4.4	5318	3	ABT04777	Abt04777 C parvum
36	53.6	4.3	5318	2	AAV20701	Aav20701 Cryptospor
C 37	53.2	4.3	3111	8	ACA40105	Aca40105 Prokaryot
C 38	49.4	4.0	7758	6	ABL33102	Ab133102 Human imm
39	48.8	3.9	110000	12	ADH69807	Adh69807 Human vbe
40	48.6	3.9	267156	6	ABL68560	Ab168560 Kidney ca
41	48.6	3.9	424	2	AAT29067	Aat29067 Probe for
C 42	47	3.8	1893	8	ACA28989	Aca28989 Prokaryot
C 43	47	3.8	48551	6	AAS20800	Aas20800 Clostridi
44	45.8	3.7	3567	3	AAA70117	Aaa70117 Plasmodiu
45	45.6	3.7	1830	6	ABL56243	Ab156243 AmBPV met

ALIGNMENTS

RESULT 1

AA62305
ID AAD62305 standard; DNA; 3786 BP.

XX AAD62305;

DT 15-JAN-2004 (first entry)

DE Candida albicans agglutinin-like sequence (ALS) 1 gene.

XX Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;
KW candidiasis; vaccine; fungicide; gene; ss.

XX Candida albicans.

PH Key Location/Qualifiers
CDS 1..3783

FT /*tag= a
FT /product= "C. albicans ALS protein"
FT /codon= (seq:"ctg", aa:Ser)

XX US2003124134-A1.

XX 03-JUL-2003.

XX 13-SEP-2002; 2002US-00245802.

XX 19-NOV-1999; 99US-0166663P.

XX 18-NOV-2000; 2000US-00715876.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Edwards JE, Filler SG, Sheppard DC, Ibrahim A, Fu Y;

XX WPI; 2003-810971/76.

XX P-PSDB; ABW01168.

XX New monoclonal antibody against Candida albicans agglutinin-like sequence
PT 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
PT candidiasis, or to generate an immune response that blocks adherence of
PT the organism.

XX Disclosure; Page 12-14; 65pp; English.

XX CC The present invention relates to a monoclonal antibody against an
CC agglutinin-like sequence (ALS)1 protein that specifically binds an
CC epitope in an N-terminal domain and which inhibits adherence of Candida
CC albicans to endothelial cells. The invention is useful as vaccines for
CC treating and preventing disseminated candidiasis and for generating an
CC immune response capable of blocking adherence of the organism. The
CC invention is also useful in gene therapy. The present sequence is Candida
CC albicans agglutinin-like sequence (ALS) gene
XX SQ Sequence 3786 BP; 1170 A; 899 C; 592 G; 1125 T; 0 U; 0 Other;
Query Match. 100.0%; Score 1245; DB 10; Length 3786;
Best Local Similarity 100.0%; Pred. No. 1.4e-287;
Matches 1245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCAATCACTGGTGTGTTTGTAGATGTTTAAATTCATTAACCTGGTCCAATGCTGCTAAT 60
DB 52 AAGCAATCACTGGTGTGTTTGTAGATGTTTAAATTCATTAACCTGGTCCAATGCTGCTAAT 111
QY 61 TATGCTTTCAAAGGCCAGGATACCCAACTTGGAACTGCTGTTTGGGTGCTCTTAGAT 120
DB 112 TATGCTTTCAAAGGCCAGGATACCCAACTTGGAACTGCTGTTTGGGTGCTCTTAGAT 171
QY 121 GGTACCAAGTGCATCCAGGGGATACATTCACATTTGAATATGCCATGTGTGTTTAAATAT 180
DB 172 GGTACCAAGTGCATCCAGGGGATACATTCACATTTGAATATGCCATGTGTGTTTAAATAT 231
QY 181 ACTACTTCAAACAATCTGTGTTGTTAACTGCGGATGGTGTAAATATGCTACTGTGCAA 240
DB 232 ACTACTTCAAACAATCTGTGTTGTTAACTGCGGATGGTGTAAATATGCTACTGTGCAA 291
QY 241 TTTTATTTCTGGTGAAGAAATTCACAACTTTTTCATTAACATGCTACTGTGAACGCGCT 300
DB 292 TTTTATTTCTGGTGAAGAAATTCACAACTTTTTCATTAACATGCTACTGTGAACGCGCT 351
QY 301 TTGAAATCATCATTAAGGCAATTTGGTACAGTTACTTTTACCATTTGCAATTTCAATTTGGT 360
DB 352 TTGAAATCATCATTAAGGCAATTTGGTACAGTTACTTTTACCATTTGCAATTTCAATTTGGT 411
QY 361 GGAACAGGTTCACTCACTGATTTGGGAAGATCTTAAATGTTTACTGCTGGTACCAATACA 420
DB 412 GGAACAGGTTCACTCACTGATTTGGGAAGATCTTAAATGTTTACTGCTGGTACCAATACA 471
QY 421 GTCACTTTAATGATGTGTATAGATATCTCAATTCATGTTGAGTTTGAAGAGTCAACC 480
DB 472 GTCACTTTAATGATGTGTATAGATATCTCAATTCATGTTGAGTTTGAAGAGTCAACC 531
QY 481 GTTGATCCAAGTGCATATTTGTATGCTTCCAGAGTTATGCCAAGTCTCAATAAGGTCACA 540
DB 532 GTTGATCCAAGTGCATATTTGTATGCTTCCAGAGTTATGCCAAGTCTCAATAAGGTCACA 591
QY 541 ACTCTTTTGTGGCACCACATGTAAGAAATGGTTTACACATCTGGTACAAATGGGGTTCTCC 600
DB 592 ACTCTTTTGTGGCACCACATGTAAGAAATGGTTTACACATCTGGTACAAATGGGGTTCTCC 651
QY 601 AGTAGTAACGCTGACGTTGCTATTGATTTGCTCAATATTCATATTTGTTATCACAAAAGGA 660
DB 652 AGTAGTAACGCTGACGTTGCTATTGATTTGCTCAATATTCATATTTGTTATCACAAAAGGA 711
QY 661 TTAATGATTTGAATTTATCCGGTTTTCATCTGAATCATTTAGTTACATAAACTTTGTACA 720
DB 712 TTAATGATTTGAATTTATCCGGTTTTCATCTGAATCATTTAGTTACATAAACTTTGTACA 771
QY 721 TCTAATGGAATTCAGATTAATATCAAAATGATCTGCTGTTATCTGCTCAATTTATTTGAT 780
DB 772 TCTAATGGAATTCAGATTAATATCAAAATGATCTGCTGTTATCTGCTCAATTTATTTGAT 831
QY 781 GCTTATATTTCTGCTACAGATGTTTAAACCAATATATCTTTAGCATATACCAATGATTATCT 840
DB 832 GCTTATATTTCTGCTACAGATGTTTAAACCAATATATCTTTAGCATATACCAATGATTATCT 891
QY 841 TGTGCTGGCAGTCTGCTGCAAAAGTAAACCTTTTCACTTTAAGATGCACTGGATACAAGAA 900

DB 892 TGTGCTGGCAGTCTGCTGCAAAAGTAAACCTTTTCACTTTAAGATGGACTGGATACAAGAA 951
QY 901 AGTGATGCCGGATCTAAACGGTATTGTTCATTGTTGCTTACAACTAGAACAGCTTACAGACAGT 960
DB 952 AGTGATGCCGGATCTAAACGGTATTGTTCATTGTTGCTTACAACTAGAACAGCTTACAGACAGT 1011
QY 961 ACCACTGCTGTCACTACTTTCACCATTCATCCAAAGTGTGTGATAAAACCAAAACCAATCGAA 1020
DB 1012 ACCACTGCTGTCACTACTTTCACCATTCATCCAAAGTGTGTGATAAAACCAAAACCAATCGAA 1071
QY 1021 ATTTGCCAACTTATTCACCACTACCATCACAACTTCATATGTTGGTGTGACTACTTCC 1080
DB 1072 ATTTGCCAACTTATTCACCACTACCATCACAACTTCATATGTTGGTGTGACTACTTCC 1131
QY 1081 TATCTGACTAAGACTGSCACCAATTTGGTGAACACAGCTACTGTTTATTGTTGATGTCATAT 1140
DB 1132 TATCTGACTAAGACTGSCACCAATTTGGTGAACACAGCTACTGTTTATTGTTGATGTCATAT 1191
QY 1141 CATACTACCACAACTGTTTACCAGTGAATGGACAGGAACAAATCATCTACCAACCAACTCGT 1200
DB 1192 CATACTACCACAACTGTTTACCAGTGAATGGACAGGAACAAATCATCTACCAACCAACTCGT 1251
QY 1201 ACCAATCCAACTGATTCAAATTCACACAGTGGTGGTACAAAGTTCCA 1245
DB 1252 ACCAATCCAACTGATTCAAATTCACACAGTGGTGGTACAAAGTTCCA 1296
RESULT 2
AAD62309
ID AAD62309 standard; DNA; 3813 BP.
XX
XX AAD62309;
XX
DT 15-JAN-2004 (first entry)
XX
DE Candida albicans agglutinin-like sequence (ALS) 5 gene.
XX
KW Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;
KW candidiasis; vaccine; fungicide; gene; ss.
XX
OS Candida albicans.
FH Key
FT CDS 1. .3813
FT /*tag= a
FT /product= "C. albicans ALS protein"
FT /codon= (seq:"ctg", aa:Ser) /codon= (seq:"ttg", aa:Tyr)
XX
US2003124134-A1.
XX
PD 03-JUL-2003.
XX
XX 13-SEP-2002; 2002US-00245802.
XX
XX 19-NOV-1999; 99US-0166663P.
XX 18-NOV-2000; 2000US-00715876.
XX
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
XX Edwards JB, Fuller SG, Sheppard DC, Ibrahim A, Fu Y;
XX WPI; 2003-810971/76.
XX P-PSDB; ABW01172.
XX
XX New monoclonal antibody against Candida albicans agglutinin-like sequence
PT 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
PT candidiasis, or to generate an immune response that blocks adherence of
PT the organism.
XX
XX Disclosure; Page 26-27; 65pp; English.
XX
XX The present invention relates to a monoclonal antibody against an

CC albicans to endothelial cells. The invention is useful as vaccines for
CC treating and preventing disseminated candidiasis and for generating an
CC immune response capable of blocking adherence of the organism. The
CC invention is also useful in gene therapy. The present sequence is Candida
CC albicans agglutinin-like sequence (ALS) gene
XX
SQ Sequence 4383 BP; 1359 A; 922 C; 705 G; 1397 T; 0 U; 0 Other;

Query Match 76.2%; Score 949; DB 10; Length 4383;
Best local Similarity 85.1%; Pred. No. 9.5e-217;
Matches 1060; Conservative 0; Mismatches 185; Indels 0; Gaps 0;

QY 1 AAGCAATCACTGGTGTGTTTGAATGATGTTTAAATTCATTAACTTGGTCCAAATGCTGCTAAT 60
DB 748 AAGCAATCACTGGTGTGTTTCAACAGTTTAAATTCATTGACTTGGTCTAATGCTGCTACT 807
QY 61 TATGCTTTCAAGGGCCAGGATACCCAACTTGGAATGCTGTTTGGTGGTCTCTTAGAT 120
DB 808 TATCATTTAAGGGACCCAGGAACCCCACTTGGAAATGCTGTTTGGGTGGTCTTTAGAT 867
QY 121 GGTACCAAGTCCCAATCCAGGGGATACATTCACATTTGAATATGCCATGTGTTTAAATAT 180
DB 868 GGTACTAGTGCAAGTCCGGGAGATACATTCACATTTGAATATGCCATGTGTTTAAATTT 927
QY 181 ACTACTTTCACAAATCATCTGTTGATTTAACTGCCGATGGTGTAAATATGCTACTTGTCAA 240
DB 928 ACTACTTTCACAAATCATCTGTTGATTTGACTGCTCATGCTGTTAAATATGCTACATGTCAA 987
QY 241 TTTTAAATCTGGTGAAGAAATTCACAACTTTTTCATATTAACATGATCTGTGAACGGCT 300
DB 988 TTTTCAGGCGAGTGAAGAAATTTATGACCTTTTACATTAACATGATCTGTGAGCAATACT 1047
QY 301 TTGAATTCATCCATTAAGGCAATTTGGTACAGTTACTTTTACCAATGCAATCAATGTTGGT 360
DB 1048 TTGACTCCATCTATTAAGGGCTTTGGGTACTGTACCTTACACCTTGCAATTCATTAATGAGT 1107
QY 361 GGAACAGGTTTCATCAACTGATTTTGAAGATTTCAAATGTTTAACTGCTGGTACCAATPACA 420
DB 1108 GGAACAGGTTTCATCAACTGATTTTGAAGATTTCAAATGTTTAACTGCTGGTACTAACACA 1167
QY 421 GTCACTTTAATGATGATGAATAAGATATCTCAATGATGTTGAGTTGAAAGTCAACC 480
DB 1168 GTTACATTTAATGATGATGATGAATAAGATATCTCAATGATGTTGAGTTGAAAGTCAAAAT 1227
QY 481 GTTACATCAAGTGCATATTTGATGCTTCCAGAGTATGCAAGTCTCAATAAGGTCAACA 540
DB 1228 GTGATCCAAAGGGTCTTAACATGATTCAGAGTTATACCAAGTCTCAACAAGTGTCA 1287
QY 541 ACTCTTTTGTGGCCACCAATGTGAAAATGGTTTACACATCTGGTCAATGGGGTTCTCC 600
DB 1288 ACTCTTTTGTGGCCACCAATGTGAAAATGGTTTACACATCTGGTCAATGGGGTTCTCC 1347
QY 601 AGTAGTAACGGTGAAGTGTGATTTGATGCTCAAAATATTCATATGTTGATATCACAAAGGA 660
DB 1348 AACACTTATGCTGATGTTTCAAAATGACTGTTCAAAATATTCATGTTGTTGATATCAAAAAGGA 1407
QY 661 TTAATAGTTGGAATATCCGGTTTTCATCTGAATCAATTTAGTTACACTAAACTTTGATCA 720
DB 1408 TTGAATGATTTGGAATATCCGGTTTTCATCTGAATCAATTTAGTTACACTAAACTTTGATCA 1467
QY 721 TCTAATGGAATTCAGATTTAAATATCAAAATGTATCTGCTGTTATCTGCCATTTATTTGAT 780
DB 1468 TCTAATGGAATTCAGATTTAAATATCAAAATGTATCTGCTGTTATCTGCCATTTATTTGAT 1527
QY 781 GCTTATATTTCTGCTACAGATGTTTAAACCAATATATCTTTAGCATATACCAATGATTATCT 840
DB 1528 GCTTATATTTCTGCTACAGATGTTTAACTCGTACACCTTGTGTTATGTTAATGATATACT 1587
QY 841 TGTCTGCGAGTCTGCTGCAAGTAAACCTTTTCACTTTTAAGATGCACTGGATACAAGAAT 900
DB 1588 TGTCTGCTGTTTATGTCGACAGTGCACCTTTTCAATTTAAGATGCACTGGATACAAGAAT 1647
QY 901 AGTGATGCCGATCTAAACGGTATTTGTTGATTTGCTGTACAACTAGAACAGTTTACAGACAGT 960

DB 1648 AGTGATGCTGGATCTAAACGGTATTTGTTATTTGGCTACTTACCAGAACAGTTTACAGACAGT 1707
QY 961 ACCACTGCTGCTCACTACTTTTACCAATTCATCCAAAGTGTGTGATAAAACCAAAACAATCGAA 1020
DB 1708 ACTACCGCGTGACCACTTACCAATTCGATCTCTTAAACCGGCAAAACTAAGACAATTGAA 1767
QY 1021 ATTTTGCACCACTTATCCAAACCACTTACCAATTCATCAATCTTATATGTTGGTGTGACTTCTCC 1080
DB 1768 ATTTTGAACCTTATCCAAACCACTTACCAATTCATCAATCTTATATGTTGGTGTGACTTCTCC 1827
QY 1081 TATCTCACTAAGAGTGCACCAATTTGGTGAACAGCTACTGTTTATTTGATGTTGCGCATAT 1140
DB 1828 TACCTGACCAAAACTGCAACCAATTTGGGGAACCTGCTACTGTTTATTTGATATTTCCATAT 1887
QY 1141 CATACTACCAACACTGTTTACCAGTGAATGGACAGGAGAACATCACTACCAACCACTCGT 1200
DB 1888 CACACTACCACTACTGTTTACCAGTGAATGGACAGGAGAACATCACTTCCACCAACAT 1947
QY 1201 ACCAATCCAACTGACTCTCAATAGACACTGTCTCATTTGTACAAGTTCCA 1245
DB 1948 ACTAATCCAACTGACTCTCAATAGACACTGTCTCATTTGTACAAGTTCCA 1992

RESULT 4

AAD62307

ID AAD62307 standard; DNA; 3360 BP.

XX AAD62307;

XX 15-JAN-2004 (first entry)

XX Candida albicans agglutinin-like sequence (ALS) 3 gene.

XX Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;

XX candidiasis; vaccine; fungicide; gene; ss.

XX Candida albicans.

XX Key Location/Qualifiers

XX CDS 1..3783

XX FT /*tag= a

XX FT /product= "C. albicans ALS protein"

XX FT /codon= (seq:"ctg", aa:Ser)

XX PN US2003124134-A1.

XX PD 03-JUL-2003.

XX 13-SBP-2002; 2002US-00245802.

XX 19-NOV-1999; 99US-0166663P.

XX 18-NOV-2000; 2000US-00715876.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Edwards JE, Filler SG, Sheppard DC, Ibrahim A, Fu Y;

XX WPI; 2003-810971/76.

XX P-PSDB; ABW01170.

XX New monoclonal antibody against Candida albicans agglutinin-like sequence
PT 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
PT candidiasis, or to generate an immune response that blocks adherence of
PT the organism.

XX Disclosure; Page 19-21; 65pp; English.

XX The present invention relates to a monoclonal antibody against an
CC agglutinin-like sequence (ALS)1 protein that specifically binds an
CC epitope in an N-terminal domain and which inhibits adherence of Candida
CC albicans to endothelial cells. The invention is useful as vaccines for
CC treating and preventing disseminated candidiasis and for generating an

CC immune response capable of blocking adherence of the organism. The
CC invention is also useful in gene therapy. The present sequence is Candida
CC albicans agglutinin-like sequence (ALS) gene
XX

SQ Sequence 3360 BP; 1029 A; 804 C; 520 G; 1007 T; 0 U; 0 Other;

Query Match 76.1%; Score 947.4; DB 10; Length 3360;
Best Local Similarity 85.1%; Pred. No. 2.1e-216;
Matches 1059; Conservative 0; Mismatches 186; Indels 0; Gaps 0;

Qy	1	AAGACAATCACTGGTGTGTTTGAATGTTTAAATCAATTAACCTGTGTCOAATGCTGCTAAT	60
Db	52	AAGACAATCACTGGTGTGTTTCAACAGTTTTAAATCAATTAACCTGTGTCOAATGCTGCTAAT	111
Qy	61	TATGCTTTCAAGGCGCAGGATACCAACTTGGATGCTGTTTGGGTTGGTCTTATAGAT	120
Db	112	TATAATTAAGGGACACAGGAAACCCCACTTGGAAATGCTGTTTGGGTTGGTCTTATAGAT	171
Qy	121	GGTACAGTGCCTAATCCAGGGGATACATTCATTAATGAATATGCCATGTGTGTTTAAATAT	180
Db	172	GGTACTAGTGCAGTCCGGAGATACATTCATTAATGAATATGCCATGTGTGTTTAAATAT	231
Qy	181	ACTACTTCACAAATCTGTTGATTTAACTGCCGATGGTGTAAATATGCTACTTGTCAA	240
Db	232	ACTACTTCACAAATCTGTTGATTTGATTTGATGCTGCTCATGCTGTGTTAAATATGCTACTGCTCAA	291
Qy	241	TTTTATTCTGGTGAAGATTCACAACTTTTCTACATTAACATGCTACTGTAACGCGCT	300
Db	292	TTTTCAGGCGAGTGAAGATTTATGACCTTTTCTACATTAACATGCTACTGTAACGCGCT	351
Qy	301	TTGAAATCATCATTAAGGCAATTTGCTCAGTTCATTTACCAATTTGCAATTCATGTTGGT	360
Db	352	TTGATCTCATCTATTAAGGCTTTGGGTACTGCTACTTACCACTTGGATTCATGTTAGGT	411
Qy	361	GGACAGGTTCATCAACTGATTTGGAAGATTCCTAAATGTTTACTGCTGGTACCAATACA	420
Db	412	GGAACTGGTTCCTCTGTTGATTTGGAAGATTCCTAAATGTTTACTGCTGGTACTAACACA	471
Qy	421	GTACATTTAATGATGGTGATTAAGATATCTCAATGATGTTGATTTGAAAGTCACCC	480
Db	472	GTACATTTAATGATGGTGATTAAGATATCTCTATTAATGTTGATTTGAAAGTCACCAAT	531
Qy	481	GTTGATCCAAAGTGCATATTTGATGCTTCCAGATTTATGCCAAGTCTCAATTAAGGTACA	540
Db	532	GTCGATCCAAAGGCTACTTAATGATTTCCAGATTTATGCCAAGTCTCAATTAAGGTACA	591
Qy	541	ACTCTTTTGTGGCCACCAATGTGAAATGGTTACATCTGGTACCAATGGGTTCTCC	600
Db	592	ACTCTTTTGTGGCCACCAATGTGAAATGGTTACATCTGGTACCAATGGGTTCTCGCT	651
Qy	601	AGTAGTACGGTGACGTTGCTATTGATGCTCAATATTCATATTGGTATCAACAAAGGA	660
Db	652	AAACACTTATGTTGATGTTCAAAATGCTGTTCAAAATATTCATGTTGGTATTAACAAAGGA	711
Qy	661	TTAAATGATGGAAATATCCGGTTTCATCTGAATCATTTAGTTACACTAAAATTTGTACA	720
Db	712	TTGAATGATGGAAATATCCGGTTTCATCTGAATCATTTAGTTACACTAAAATTTGTACA	771
Qy	721	TCTAATGGAATTCAGATTAATATCAAAATGCTGCTGCTGTTATCGTCCATTTATGAT	780
Db	772	TCTAATGGAATTCAGATTAATATCAAAATGCTGCTGCTGTTATCGTCCATTTATGAT	831
Qy	781	GCTTATATTTCTGCTACAGATGTTTAAACCAATATATCTTTAGCATATACCAATGATTACT	840
Db	832	GCTTATATTTCTGCTACAGATGTTTAAATTCGTTACACCTGCTGCTATGCTAATGAATATACT	891
Qy	841	TGTCCTGGCAGTCCGCTCGCAAGTAAACCTTTCACTTTAAGATGCACTGGATACAGAAAT	900
Db	892	TGTGCTGGTGGTTATTTGGCAACGTCGACCTTTTCAATTAAGATGCACTGGATACAGAAAT	951
Qy	901	AGTGATGCCGGATCTAAACGGTATTTGCTATTGTTGCTTACCACTAGAACAGTTACAGACAGT	960
Db	952	AGTGATGCCGGATCTAAACGGTATTTGTTATTTGTTGGCTACTACCAAGAACAGTTACAGACAGT	1011

Qy	961	ACCATGCTGCTACTTTTACCAATTCAAAGTGTGTGATAAAACCAAAACAATCGAA	1020
Db	1012	ACTACCGCTGTGACCACCTTACCAATTCGATCTCTACCGGACAAAACCTAAGCAATCGAA	1071
Qy	1021	ATTTTGAACCTATTTCCAAACACTTACCAATTCATCAATCTTATGTTGGTGTGACTACTTCC	1080
Db	1072	ATTTTGAACCTATTTCCAAACACTTACCAATTCATCAATCTTATGTTGGTGTGACTACTTCC	1131
Qy	1081	TATCTGCTAGACTGCGACCAATTTGGTGAACAGCTACTGTTATTGTTGATGTGCCATAT	1140
Db	1132	TACTGTACCAAACTGCAACCAATTTGGGAAACTCTCTACTGTTATTGTTGATTTCCATAT	1191
Qy	1141	CATATCTACCACTGTTTACCAAGTGAATGGACAGCAATCACTTACCAACCAACTCGT	1200
Db	1192	CACACTACCACTGTTTACCAAGTGAATGGACAGCAATCACTTACCAACCAACTCGT	1251
Qy	1201	ACCAATCCAACTGATTCATTTGACACAGTGGTGTGACAGTTCCA	1245
Db	1252	ACTAATCCAACTGATTCATTTGACACAGTGGTGTGACAGTTCCA	1296

RESULT 5

AAD62306
ID AAD62306 standard; DNA; 1404 BP.

XX AAD62306;

DT 15-JAN-2004 (first entry)

XX Candida albicans agglutinin-like sequence (ALS) 2 gene.

XX Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;

KW candidiasis; vaccine; fungicide; gene; ss.

XX Candida albicans.

PH Key Location/Qualifiers

CDS 1..1404

FT /+tag= a

FT /product= "C. albicans ALS protein"

FT /transl_except= {pos:121..123, aa:Lys}

FT /codon= (seq: "ctg", aa:Ser)

FT /note= "No stop codon"

FT /partial

XX US2003124134-A1.

XX 03-JUL-2003.

XX 13-SEP-2002; 2002US-00245802.

XX 19-NOV-1999; 99US-0166663P.

PR 18-NOV-2000; 2000US-00715876.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Edwards JE, Filler SG, Sheppard DC, Ibrahim A, Fu Y;

XX WPI; 2003-810971/76.

DR P-PSDB; AEW01169.

XX New monoclonal antibody against Candida albicans agglutinin-like sequence
PT 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
PT candidiasis, or to generate an immune response that blocks adherence of
PT the organism.

XX Disclosure; Page 17-18; 65pp; English.

XX The present invention relates to a monoclonal antibody against an

CC agglutinin-like sequence (ALS)1 protein that specifically binds an

CC epitope in an N-terminal domain and which inhibits adherence of Candida

CC albicans to endothelial cells. The invention is useful as vaccines for

CC treating and preventing disseminated candidiasis and for generating an
CC immune response capable of blocking adherence of the organism. The
CC invention is also useful in gene therapy. The present sequence is Candida
CC albicans agglutinin-like sequence (ALS) gene
XX

Query Match	71.9%	Score 895;	DB 10;	Length 1404;
Best local Similarity	83.2%;	Pred. No. 5.7e-204;		
Matches 1031;	Conservative 0;	Mismatches 205;	Indels 3;	Gaps 17;
Qy	7	ATCACTGGTGTGTTTTGATAGTTTTAAATTCATTAACCTGGTCCAAATGCTGCTAAATATATGCT	66	
Db	58	ATTACGGGTGTTTTCAATAGTTTTGATTCGTTGACATGGAACAAGAGCTGGTAATATGCT	117	
Qy	67	TTCAAAAGGCGCAGGATACCCAACTTGGAAATGCTGTTTTGGGTGGTCTCTTAGATGGTACC	126	
Db	118	TATAACGGCCCCAAATAGACCAACTTGGAAATGCTGTTTTGGGCTGGTCTTTAGATGGTACT	177	
Qy	127	AGTCCCAATCCAGGGGATACATTCACATTTGAATATGCCATGTGTGTTTTAAATATATACTACT	186	
Db	178	AGTGCAATCCAGGAGACACATTCACATTTGAATATGCCATGTGTGTTTTAAATATATACTACT	237	
Qy	187	TCACAAACATCTGTTGATTTAACTGCCGATGGTGTAAATATGCTACTTGTCAAATTTTAT	244	
Db	238	GATCAAAACATCTGTTGATTTGACTGCTCAAGGTGTAAATATGCTACTACTGTCAGTTTTAT	297	
Qy	247	TCTGGTGAAGAAATTCACAACTTTTCTATCATTAACATGTACTGTGGAAACGACGCTTTGAA	306	
Db	298	TCAGGTGAAGAAATTTACAAACATTTCTTCATTTAAATATGTACTGTGAGCAATACTTTAACA	357	
Qy	307	TCATCTATTAAAGGCAATTTGGTACAGTTACTTTTACCATTTGCATTCATTAATGTTGGTGAACA	366	
Db	358	TCATCTATTAAAGCTTTGGGTACGGTTACTTTTACCAATTTCAATTAATGTTGGTGAACA	417	
Qy	367	GGTTCATCAACTGATTTGGGAGATTCCTAAATGTTTTTACTGCTGGTACCAATACAGTCAACA	426	
Db	418	GGTTCATCGGTTGATTTGGGAAAGTTCTCAATGTTTTTAAAGGCTGGCAACCAACAGATTTACT	477	
Qy	427	TTTAAATGATGTGTATAAGATATCTCAATGATGTTTGAGTTTGAAAGTCAACCGTTCAT	486	
Db	478	TTTTAATGATGTGTATAAGAAATCTCAATGATGCTGTTGATTTGAGTTTGAAAGTCAACCGTTCAT	537	
Qy	487	CCAAGTGCATATTTGTATGCTTCCAGAGTTATGCGCAAGTCTCAATTAAGGTCAACACTCTT	546	
Db	538	GCAAGTGGATATTTTCATAGCGTCAAGA CTATTATCCAAAGTATTAACAAGATTTCAATCACT	597	
Qy	547	TTTGTGGCACCAACATGTGAAATGGTTTACATCTGTTTCAATCGGGGTTCTCCAGTAGT	606	
Db	598	TATGTGGCACCAACATGTGCAATGGCTTACATCTGGTGCATGGGGTTCTATGTTCTC	657	
Qy	607	AACGGTGCAGTTGCTTATTTGATTTGCTTCAAAATATTCATATTTGGTATCACAAAGGATTAAT	666	
Db	658	ACTGGTGACACTACTATTGACGTTTCAATGTTTCATGTTGGTATTTACAAAGGATTAAT	717	
Qy	667	GATTGGAATATATCCGGTTTCATCTGAAATCATTTAGTTTACACTAAAACCTTTGACATCTAAT	726	
Db	718	GATTGGAATATTTCCGGTATCGTCTGATTCATTTAAGTTTCAATTAAGTATTTGTTTCACTACA	777	
Qy	727	GGAAATTCAGATTTAAATATCAAAATGCTACTGCTGGTTATCGTCCCACTTTATTCATGCTTAT	786	
Db	778	GGTATTTCTATCAATATGAAGAAATGCTCCCGCTGGTATCGTCCATTTTGGACGTATAT	837	
Qy	787	ATTTCTGCTACAGATGTTTAAACCAATATATCTTTAGCATATATCAATGATATATCTTTGCTCT	846	
Db	838	ACTCTGGTGTCAAGGCCAGAACAGACA-----ATTAAGATATATCAATTAAGTATTTCCCTGTGTT	894	
Qy	847	GGCAGTCTGTCGAAGTAAACCTTTTCACTTTTAAAGTGGACTGGGATACAAAGAAATAGTAT	906	
Db	895	GGTAGTTCCTTCAAGTAAGCCGTTTCAATTTTAAAGTTGAGAGGATACATTAATATAGTGA	954	
Qy	907	GCCGGATCTAACCGGTATTTGTCTATTTGTTGCTACAACTTAGAACAGTTTACAGACAGTACCCT	966	

Db	955	GCTAAATCTCAACGGTTTTGTGCATTTGTGCTACAACCCGACAGTACTACTGACAGCTACTACT	101
Qy	967	GCTGTCACTACTTTTACATTCAAATCCAAAGTGTGATAAAACCAAAACAATCGAAATTTTG	1026
Db	1015	GCTGTCACTACTTTTACCTTTTAAATCCAAAGTGTGTGACAAAACCAAAACAATCGAAATTTTG	1074
Qy	1027	CAACCTATTCCAAACCACTACCATCAACAACCTTCATATGTTGGTGTGACTCTTCCTATCTG	1086
Db	1075	CAACCTATTTCACCAACCAACATCAACAATTCATATGTTGGTGTGACTACTTCTCTACCTG	1134
Qy	1087	ACTAAGACTGCACCAATTTGGTGAAACAGCTACTGTGTTATTGTTGGATGTGCCATATCATACT	1146
Db	1135	ACTAAAACCTGCACCAATTTGGTGAAACAGCTACTGTGTTATTGTTGGATGTGCCATATCATACT	1194
Qy	1147	ACCACAACTGTTACCGTGAATCGACAGGAACAATCACTACCACCAACAACCTCGTACCAAT	1206
Db	1195	ACCACAACTGTTACCGTGAATCGACAGGAACAATCACTACCACCAACAACCTCGTACCAAT	1254
Qy	1207	CCAACTGAATCAATTTGACACAGTGGTGGTACAAGTTCCA	1245
Db	1255	CCAACTGAATCTATAGATACTGTGCTGTTGTCGAAGTTCCA	1293

RESULT 6	
AD62308	
ID	AD62308 standard; DNA; 1407 BP.
XX	
AC	AD62308;
XX	
DT	15-JAN-2004 (first entry)
XX	
DE	Candida albicans agglutinin-like sequence (ALS) 4 gene.
XX	
KW	Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;
KW	candidiasis; vaccine; fungicide; gene; ss.
XX	
OS	Candida albicans.
XX	
FT	Location/Qualifiers
FT	1. 1407
CDS	/*tag= a
FT	/product= "C. albicans ALS protein"
FT	/codon= (seq: "ctg", aa:Ser)
FT	/note= "No stop codon"
FT	/partial
FT	

XX	US2003124134-A1.
PN	
XX	
XX	03-JUL-2003.
XX	
XX	13-SEP-2002; 2002US-00245802.
XX	
XX	19-NOV-1999; 99US-0166663P.
PR	
PR	18-NOV-2000; 2000US-00715876.
XX	
XX	(HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX	
PI	Edwards JE, Filler SG, Sheppard DC, Ih
XX	
XX	WPI; 2003-810971/76.
DR	
DR	P-PSDB; ABW01171.

XX New monoclonal antibody against *Candida albicans* agglutinin-like sequence
PT 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
PT candidiasis, or to generate an immune response that blocks adherence of
PT the organism.
XX
XX Disclosure; Page 24; 65pp; English.
PS
XX
XX The present invention relates to a monoclonal antibody against an
CC agglutinin-like sequence (ALS)1 protein that specifically binds an
CC epitope in an N-terminal domain and which inhibits adherence of *Candida*
CC *albicans* to endothelial cells. The invention is useful as vaccines for

CC treating and preventing disseminated candidiasis and for generating an
CC immune response capable of blocking adherence of the organism. The
CC invention is also useful in gene therapy. The present sequence is Candida
CC albicans agglutinin-like sequence (ALS) gene
XX
SQ

Sequence 1407 BP; 391 A; 294 C; 253 G; 469 T; 0 U; 0 Other;

Query Match 58.9%; Score 733.4; DB 10; Length 1407;
Best Local Similarity 74.5%; Pred. No. 2.6e-165;
Matches 923; Conservative 0; Mismatches 316; Indels 0; Gaps 0;

QY 7 ATCACTGCTGTTTGTAGTATTAATTCATTAATCTGGTCCCAATGCTGCTAAATATGCT 66
DB 58 ATTACAGGTGTTTCAATAGTATTAATTCGTTAACTTGGGCCAATGCTGCTTCTTATCCA 117
QY 67 TTCAAAGGCCAGGATACCCCACTGGATGCTGTTTGGGTGCTCTAGAGTGAACC 126
DB 118 TATAGAGGTCCAGCTACTCTCTACTTGGACCGCTGTAATAGGATGGTCTTTAGATGGAGCT 177
QY 127 AGTGCCATCCAGGGGATACATTCACATTTGAATATGCCATGCTGTTTAAATATATACTACT 186
DB 178 ACTGCTAGTGTGGTGACACATTCAGGTTAGACGCTTGTGTTTCAAAATTTATCT 237
QY 187 TCACAAACATCTGTTGATTTAACTGCCGATGGTGTAAATATGCTACTTGTCAATTTAT 246
DB 238 GATCAAAAGCTCAATTTAGTTGCTGATGCTGCTACTTATGCTACTTGTAAATTTGAAT 297
QY 247 TCTGTTGAAGATTCACAACTTTTCTACATTAACATGCTACTGTGAACGAGCTTTGAA 306
DB 298 TCTGCCGAAGATTTTACTACTTTTCTAGTGTGTCATGCTACTGTGACTACTACAAATGACT 357
QY 307 TCATCCATTAAGGATTTGGTACTAGTTACTTTTACCATTTGATTCATCAATGTTGGGAACA 366
DB 358 GCTGACACCAAGCCATAGGAACCTGTAACATTTACCTTTCTATTCAAGTGGGGGATCA 417
QY 367 GGTTCATCACTGATTTTGGGAAGATTTCTAAATGTTTACTGCTGGTACCAATACAGTACCA 426
DB 418 GGTTCAGATGTTGATTTGGCAATTTCTCAATGTTTACTGCGAGGAATCAATACAGTTACT 477
QY 427 TTTAATGATGTTGATTAAGATATCTCAATGATGTTGATGTTGTTGAAAGTCAACCGTTGAT 486
DB 478 TTTAATGATGTTGATGATAGATTTTCCCAACAGTGTGATTTTGAATAATCAACCGTGGCC 537
QY 487 CCAAGTGCATATTTGATGCTTCCAGAGTTATGCCAGTCTCAATTAAGTCCACACTCTT 546
DB 538 TCCAGCGATCGTATCTGTTGTCAAGAAATTTTACCAGTCTTTTCAAGACGATTAATCTT 597
QY 547 TTTGTGGCACCAATGTTGAAATGTTTACACATCTGGTACAAATGGGGTCTTCCAGTACT 606
DB 598 TTTCTTCCCAAGATGTTGCAATGTTTATCTTCTGTTACAAATGGGATTTTGGACTGCT 657
QY 607 AACGGTGAAGTGTGATGTTGATGTTCAATATTTCAATATTTGTTATCAACAAAGGATTAAT 666
DB 658 GGTACTGTTGCTACTATAGATGTTTCCAGTTCATGTCGGGATATCAATGGGTTGAAT 717
QY 667 GATTGGAATATCCGGTTTCTCTGATCAATTTAGTTTACACTTAAACCTGTACTCTAAT 726
DB 718 GATTGGAATATCCAAATTTCTCTGGAATCTTTTCTTACCAAGACCTGTACTACCA 777
QY 727 GGAATTCAGATTAATATCAAAATGTTACTGCTGTTATCGTCCATTTTATGATGCTTAT 786
DB 778 AGTGTTTTATGTTAACTTTTCAAAATGTTCTGCGGATATCGTCCATTTTGTGATGCTTAT 837
QY 787 ATTTCTGCTACAGATGTTTAAACCAATATATCTTTAGCATATACCAATGATTTACTTTGCT 846
DB 838 ATTTCTGCAACAGGATGCTCATATCCATGCAATACACTTAATATATATGTTGTTGTT 897
QY 847 GGCAGTCTGTCGAAGTAAACCTTTCATTTAAGATGCACTGGATACAGATAGTAT 906
DB 898 GGCAGGCTCTCTGTTGATGACTCAATTTACTACTTCTGCGGGGATATAGTAATAGTCA 957
QY 907 GCGGATCTAACCGTATTTGCTATTGTTGCTCAACTAGAACAGTTTACAGAGTACCCT 966

DB 958 GCTGGTTCATTAATGGTATTACCAATTTGGTAAACAACAGTTACAGACAGTACCCT 1017
QY 967 GCTGTCACTACTTTTACCAATTCACCAAGTGTGTTGATATAAAACCAAAACAATCGAAATTTTG 1026
DB 1018 GCTGTGACTACTTTTACCAATTCACCAATTCGATACGACAAACCAAAACAATCGAAATTTTA 1077
QY 1027 CAACCTATTTCCAAACACTTACCATCAACATTCATATGTTGGTGTGACTACTTCTATCTG 1086
DB 1078 CAACCTATTTCCAAACACTTACCATTCACCAATTCATATGTTGGTGTGACACACTTCTACTCTG 1137
QY 1087 ACTAAGACTCGACCAATTTGGTGAACAGCTACTGTTATTTGATGTGTCATATCATACT 1146
DB 1138 ACTAAAACCTGACCAATTTGGTGAACAGCTACTGTTATTTGATGTGTCATATCATACT 1197
QY 1147 ACCAACAATCTTTACCAAGTGAATGACAGGAAACATCACTACCACCAACACTCGTACCAAT 1206
DB 1198 ACTAACAATCTTTACCAAGTGAATGACAGGAAACATTTACTACCACCAACTCGTACCAAT 1257
QY 1207 CCAACTGATTCATTAATGACAGTGGTGTACAGTTTCCA 1245
DB 1258 CCAACTGATTCATAGATCTGTTGTTTCAAGTTCCA 1296

RESULT 7

AAD62313
ID AAD62313 standard; DNA; 1404 BP.
XX
AC AAD62313;
XX
DT 15-JAN-2004 (first entry)
XX
DB Candida albicans agglutinin-like sequence (ALS) 9 gene.
XX
KW Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;
XX
OS candidiasis; vaccine; fungicide; gene; ss.
XX
FH Candida albicans.
Key Location/Qualifiers
CDS 1..1404
FT /*tag= a
FT /product= "C. albicans ALS protein"
FT /codon= (seq:"ctg", aa:Ser) /codon= (seq:"ttg", aa:Tyr)
FT /note= "No stop codon"
FT /partial
XX
US003124134-A1.
XX
03-JUL-2003.
XX
13-SEP-2002; 2002US-00245802.
XX
19-NOV-1999; 99US-0166663P.
XX
18-NOV-2000; 2000US-00715876.
XX
(HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
XX Edwards JE, Filler SG, Sheppard DC, Ibrahim A, Fu Y;
XX
XX WPI; 2003-810971/76.
XX
XX P-PSDB; ABW01176.
XX
XX New monoclonal antibody against Candida albicans agglutinin-like sequence
XX
XX 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
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XX candidiasis, or to generate an immune response that blocks adherence of
XX
XX the organism.
XX
XX Disclosure; Page 50-51; 65pp; English.
XX
XX The present invention relates to a monoclonal antibody against an
XX
XX agglutinin-like sequence (ALS)1 protein that specifically binds an
XX
XX epitope in an N-terminal domain and which inhibits adherence of Candida
XX
XX albicans to endothelial cells. The invention is useful as vaccines for

CC treating and preventing disseminated candidiasis and for generating an
CC immune response capable of blocking adherence of the organism. The
CC invention is also useful in gene therapy. The present sequence is Candida
CC albicans agglutinin-like sequence (ALS) gene
XX
SQ

Sequence 1404 BP; 413 A; 286 C; 253 G; 452 T; 0 U; 0 Other;

Query Match 57.3%; Score 713.8; DB 10; Length 1404;
Best Local Similarity 73.9%; Pred. No. 1.3e-160;
Matches 920; Conservative 0; Mismatches 322; Indels 3; Gaps 1;

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Qy 1 AAGCAATCACTGGTGTGTTGATAGTTTAAATTCATTAATCTGGTCCCAATGCTGCTAAT 60
Db 52 AAAAATATTACTGGTGTGTTTCAATAGTTTGGACTCATTCATGACATAGACTCGGTGAA 111
Qy 61 TATGCTTTCAAGGGCCAGGATACCCCAATCTGGAATGCTGTTTGGGTCCTCTAGAT 120
Db 112 TATGCTTTCAAGGGCCAGGATACCCCAATCTGGAATGCTGTTTGGGTCCTCTAGAT 171
Qy 121 GGTACCAAGTGCATCCAGGGGATACATTCACATTTGAATATGCCATGTGTGTTTAAATAT 180
Db 172 AGTACCACTGCTGACCCAGGAGACACATTCACCTTGATTTTGGCTGTGTATTAATTT 231
Qy 181 ACTACTTCACAAATCATCTGTTGATTAATTCGCCGATGGTGTAAATATGCTACTGTGCAA 240
Db 232 ATAACTACCCAAACATCTGTTGATTTGACTGCTGATGGTGTAGCTATGCCACTGTGTGAC 291
Qy 241 TTTTATTTCTGGTGAAGAAATTCACAACTTTTCTACATTAACATGATCTGTTGAACGAGCT 300
Db 292 TTTTAAATGCTGGTGAAGAAATTTACGACATTTTCTCCATTCATGATCTGTTGAACAGTGT 351
Qy 301 TTGAAATCATCCATTAAGGCAATTTGGTACAGTACTTTTACCAATTCATTCATTTGGT 360
Db 352 TCGTATCATATGCTAGGTTTCTGTTACGTTCAATTCGCTCAATTCATTCATTCATTCAT 411
Qy 361 GGAACAGGTTCATCAATCTGATTTGGAGATTCATAATGTTTACTGCTGTGATCAATACAC 420
Db 412 GGAACAGGTTCATCAATCTGATTTGGAGATTCATAATGTTTACTGCTGTGATCAATACAC 471
Qy 421 GTCAATTTAATGATGATTAAGATATCTCAATTCATTCATTCATTCATTCATTCATTCAC 480
Db 472 GTGACTTTTCAGTATGATGATTAAGATATCTCAATTCATTCATTCATTCATTCATTCAC 531
Qy 481 GTTCATCCAGTGCATATTTGTATGCTTCCAGAGTATGCAAGTTCATCAATTAAGGTACAC 540
Db 532 GTATCAACCAAGTGTATATACAGCTCAGCAATTAATTCCTAGTCTCAATTAATTCATCA 591
Qy 541 ACTCTTTTGGGCCACCAATGATGAAATGGTTTACACATCTGATCAATGGGGTCTTCC 600
Db 592 AGTCTTTTGGTGGCCACCAATGATGAAATGGTTTACACATCTGATCAATGGGGTCTTCC 651
Qy 601 AGTATGATCGGTGAGTGTGATTTGATGCTCAATATTCATATTCATATTCATACCAAGGA 660
Db 652 GCTAGTAAACGGT---GCTACTATTGATGCTCAATATTCATATTCATATTCATACCAAGG 708
Qy 661 TTAATGATGGAATTCAGATTAATATCAAAATGTAACCTGCTGTTATCGTCAATTTATGAT 720
Db 709 TTAATGATGGAATTCAGATTAATATCAAAATGTAACCTGCTGTTATCGTCAATTTATGAT 768
Qy 721 TCTAATGGAATTCAGATTAATATCAAAATGTAACCTGCTGTTATCGTCAATTTATGAT 780
Db 769 TCAACCAAGTATTAAGTGTGATTTCAAAATGTTTCCCTGCTGGTATCGCCCTTTTGTGAT 828
Qy 781 GCTTATATTTCTGCTACAGATGTTTAAACCAATATCTTTAGCATATCAATGATGATTAAT 840
Db 829 GCATATATTTCTGAGAAATATTAATGATTAATATACCTTGAGTACGCAATATGATTAAT 888
Qy 841 TGTGCTGCGAGTCTGTCGAAATGTAACCTTTTCACTTTAAGATGGAATGGAATACCAAGAT 900
Db 889 TGTGAAATGCAATATCTGTTGATGATTCATTTTCAATGCTGGGGTATATAAAC 948
Qy 901 AGTCAATGCCGATTTAAACGGTATTTGTCATTTGCTCAACTGATGAAACAGTTACAGACGT 960
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Db 949 TCTGAGCAGACCTCTGACGGGATGTGATCGTAGTTTACAAACAGACACTGTCACAGACGT 1008
Qy 961 ACCACTGCTGTCACTACTTTTACATTCATTCATTCATTCATTCATTCATTCATTCATTC 1020
Db 1009 ACAACAGCTGTGACTACTTTTCAATTCATTCATTCATTCATTCATTCATTCATTCATTC 1068
Qy 1021 ATTTGCAACCTTATTCACACCTACCATCACAATTCATTCATTCATTCATTCATTCATTC 1080
Db 1069 ATTTGCAACCTTATTCACACCTACCATCACAATTCATTCATTCATTCATTCATTCATTC 1128
Qy 1081 TATCTGACTAAGACTGCACCAATTTGGTGAACAGCTACTTCTATTCATTCATTCATTCAT 1140
Db 1129 TATGAAACATTAACCGGAACAATTTGGTGTACTGCGAGAGTCAATTCATTCATTCATTC 1188
Qy 1141 CATACTACCACTACTGTTTACCACTGATGGAACAGCTACTTCTATTCATTCATTCATTC 1200
Db 1189 CATATCACTGCCACTGTTACCAATTTCTGAGCTGGGTCAATTCATTCATTCATTCATTC 1248
Qy 1201 ACCAATCCAACTGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 1245
Db 1249 ACTAATCCCACTGGTTCCATAGACACTGTTTATTCATTCATTCATTCATTCATTCATTC 1293
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RESULT 8

AAD62310
ID AAD62310 standard; DNA; 4332 BP.

XX AAD62310;

DT 15-JAN-2004 (first entry)

XX Candida albicans agglutinin-like sequence (ALS) 6 gene.

XX Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;

XX candidiasis; vaccine; fungicide; gene; ss.

XX Candida albicans.

Key Location/Qualifiers

CDS 1..4332

FT /*tag= a

FT /product= "C. albicans ALS protein"

FT /transl_except= (pos:1..3, aa:Met)

FT /codon= (seq:"ctg", aa:Ser) /codon= (seq:"ttg", aa:Tyr)

XX US2003124134-A1.

XX 03-JUL-2003.

XX 13-SEP-2002; 2002US-00245802.

XX 19-NOV-1999; 99US-0166663P.

XX 18-NOV-2000; 2000US-00715876.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Edwards JE, Filler SG, Sheppard DC, Ibrahim A, Fu Y;

XX WPI; 2003-810971/76.

XX P-PSDB; ABW011173.

XX New monoclonal antibody against Candida albicans agglutinin-like sequence
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XX Disclosure; Page 31-33; 65pp; English.

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CC albicans to endothelial cells. The invention is useful as vaccines for
CC treating and preventing disseminated candidiasis and for generating an

CC immune response capable of blocking adherence of the organism. The
CC invention is also useful in gene therapy. The present sequence is Candida
CC albicans agglutinin-like sequence (ALS) gene

Query Match 46.2%; Score 574.6; DB 10; Length 4332;
Best Local Similarity 66.8%; Pred. No. 3.4e-127;
Matches 836; Conservative 0; Mismatches 409; Indels 6; Gaps 1;

Qy	1	AAGCAATCACTGCTGTTTTGATAGTTTAAATTTCAATTAACCTTGGTCCCAATGCTGCTAAAT	60
Db	55	AAAACTATATCGGGAGTTTTTCAAGAGTTTCAACTCATTTGACCTATATCTAATACTGGTAAC	114
Qy	61	TATGCTTTCAAAGGCGCAGGATACCCAACTTGGAAATGCTGTTTGGGTTGGTCTCTTAGAT	120
Db	115	TACCATATATGGGGTCTCTGGTTATCCAAATGGAAGTCTGCTGTTTGGGTTGGAGCTTGGAC	174
Qy	121	GGTACCAAGTGCCAATCCAGGGGATACATTTCACTATTTGAATATGCCATGTGTGTTTAAATAT	180
Db	175	GGAACTAGCTAGTCCAGGTGATACATTTTACATTTGGTCTATGCCCTCGCTTTTCAAAATTT	234
Qy	181	ACTACTTCACAAAATCTGTTTGAATTTAACTGCCGATGGTGTAAATATGCTACTTGTTCAA	240
Db	235	ATTACCAACAACTTCAGTAGACTTAATGCTTAATGGTGTCAAGTATGCAACATGTACT	294
Qy	241	TTTTTATCTGGTGAAGAAATTCACAACTTTTTTCTACATTTAACTGTACTGTGAACGACGCT	300
Db	295	TTCCATGAGGGGAAGACTTTTACTTCTTTTCAAGTATGAGTGTGTGTAGTAATAATATGGG	354
Qy	301	TTGAATCATCATTAAGGCCAATTTGGTACAGTTACTTTTACCAATGTCATTCAAATGTTGGT	360
Db	355	CTATCTTCAAATATACAGAGCGTTTGGTACCGTCAAGGTACCAATTTCAATTTCAATGTGGT	414
Qy	361	GGAACTGTTCAATCAACTGATTTGGAGAGATTTCTAAATGTTTTTACTGCTGGTACCAATACA	420
Db	415	GGAACTGGTTCATCTGTCAACATTTCAAGATTTCAAAGTGTTCATCTGCTGGAAACGACACT	474
Qy	421	GTCACTTTAATGATGGTGAATAAGATATCTCAATTTGATGTAGTTTGAATTTGAAAGTCAACC	480
Db	475	GTAACTTTTACAGACGGGATCACTAAATTTTCTACTACAGTCAATTTCCCTAAGACTCCA	534
Qy	481	GTTGATCCAAGTGCATATTTGTATGCTTCCAGAGTTATGCAAGTCTCAATTAAGGTCAACA	540
Db	535	CAATCATCTAGTCTGTGGTTTATTTTCGCAAGGGTTATTCCAAGTCTTGATAAATATATCT	594
Qy	541	ACTCTTTTGTGGCACCAATATGTAAGTGGTTTACACATCTGTGTACAAATGGGGTCTCC	600
Db	595	AGTCTTGTGTGCTTCTCAGTGTACTGCTGGATATGCAATCCGGTGTCTCGAATTTTCA	654
Qy	601	AGTAGTAACGGTGAAGTTGCTATTGATTGCTCAAAATATTCATATTTGGTATCACAAAAAGGA	660
Db	655	GCAACAAAGATGATGACAAATTTGATTTTCTACTATACATGTGGGAAATACAAATGGT	714
Qy	661	TTAAATGATTTGGAATTTCCGGTTTCATCTGAATCATTTAGTTTACACTTAAACTTTGTACA	720
Db	715	TTGATATGTTGGAATATGCCAGTATCATCAGAACTCATTTTCTTACACCAAAACTTTGTACA	774
Qy	721	TCTAATGGAATTCAGATTTAAATATCAAAATGTACTGCTGGTTATCTGTCATTTATTTGAT	780
Db	775	CCAAACAGTTTTTATTTACTTATGAAATGTTTCTCGAGGTATTCGGTCCATTTTATTTGAT	834
Qy	781	GCCTT-----ATATTTCTGCTACAGATGTAAACCAATATATCTTTAGCATATACCAATGAT	834
Db	835	TCTTACGTGAAAAAATCAGCAACAGCAAGAAATGGAATTTAATTTGAATTTACAGGATATA	894
Qy	835	TATATCTGTGCTGGCAGTCTGCTGCAAAAGTAAACCTTTTCACTTTTAAGATGGACTGGATAC	894
Db	895	TACAATTTGATGATGGCAAAAAAGGAAATGATCTCTTATATATCTTTTGGACATCATAC	954
Qy	895	AAGAAATAGTATGTCGGGATCTAAACGGTATGTGTCATTTGTGTCTGTCACAACTAGAACAGTTACA	954
Db	955	ACAAATAGTGTATGCAAGATTCOAATGGAGCTGCGGTAGTTGTTTACTTACGAGAACAGTCACT	1014

CC	albicans agglutinin-like sequence (ALS) gene																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
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```
QY 1119 TGTATTGTTGATGCGCATATCATCTACTACACCAACTGTACAGTGAATGACAGGAAC 1178
DB 100 TGTATTGTTGATGTTCCATATCACACTACACCAACTGTACTAGTGAATGACAGGAAC 41

QY 1179 AATCACTACCAACCAACTGTCACCAATCCAACTGATTCA 1218
DB 40 AATCACTACTACTACACCAAACTAATCCACAGGTTCA 1

RESULT 11
AAQ62590/c
ID AAQ62590 standard; DNA; 100 BP.
XX
AC AAQ62590;
XX
XX 25-MAR-2003 (revised)
DT 07-DEC-1994 (first entry)
XX
XX Candida albicans-specific hybridisation probe.
XX
XX DNA hybridisation probe; detection; assay; C.albicans yeast;
XX species specific sequence; ss.
XX
XX Candida albicans.
XX
XX EP595167-Al.
XX
XX 04-MAY-1994.
XX
XX 19-OCT-1993; 93EP-00116865.
XX
XX 30-OCT-1992; 92DE-04236708.
XX
XX (FARB ) BAYER AG.
XX
XX Springer W, Plempel M, Loebberding A;
XX
XX WPI; 1994-145805/18.
XX
XX New hybridisation reagents specific for Candida albicans - are
XX polynucleotide and oligo:nucleotide probes, providing high sensitivity
XX and early diagnosis of infection.
XX
XX Claim 9; Page 33; 44pp; German.
XX
XX A C.albicans gene library was prepared in pBR322 and inserts were
XX selected for multiple presence in the genome, strong conservation without
XX deletions or insertions and absolute specificity for C.albicans. Gene
XX probe 431.19 (AAQ62552) hybridised to all but 4 of the 87 clinical
XX isolates of C.albicans being tested. A clone (436.1) was then isolated
XX from the 4 isolates not recognised by 431.19. Some 100mer
XX oligonucleotides covering the complete sequences of 431.19 and 436.1 were
XX synthesised and tested (see AAQ62558-Q62594). All were found to be
XX absolutely specific for C.albicans. (Updated on 25-MAR-2003 to correct PN
XX field.)
XX
XX Claim 9; Page 33; 44pp; German.
XX
XX A C.albicans gene library was prepared in pBR322 and inserts were
XX selected for multiple presence in the genome, strong conservation without
XX deletions or insertions and absolute specificity for C.albicans. Gene
XX probe 431.19 (AAQ62552) hybridised to all but 4 of the 87 clinical
XX isolates of C.albicans being tested. A clone (436.1) was then isolated
XX from the 4 isolates not recognised by 431.19. Some 100mer
XX oligonucleotides covering the complete sequences of 431.19 and 436.1 were
XX synthesised and tested (see AAQ62558-Q62594). All were found to be
XX absolutely specific for C.albicans. (Updated on 25-MAR-2003 to correct PN
XX field.)
XX
XX Sequence 100 BP; 31 A; 17 C; 19 G; 33 T; 0 U; 0 Other;
XX
XX Query Match 6.6%; Score 82.4; DB 2; Length 100;
XX Best Local Similarity 89.0%; Pred. No. 6.5e-10;
XX Matches 89; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 919 GGTATTGTCATTGTTGCTACAACTAGACAGTTACAGACAGTACCACTGCTGTCTACT 978
DB 100 GGTATTGTCATTGTTGCTACAACTAGACAGTTACAGATAGTACTGCTGTGACTACT 41

QY 979 TTACCAATTCATCCAGTGTTCATTAACCAAAACAATCG 1018
DB 40 TTACCAATTCATCCAGTGTTCATTAACCAAAACAATG 1

RESULT 12
AAQ62589/c
ID AAQ62589 standard; DNA; 100 BP.
XX
AC AAQ62589;
XX
XX 25-MAR-2003 (revised)
DT 07-DEC-1994 (first entry)
XX
XX Candida albicans-specific hybridisation probe.
XX
XX DNA hybridisation probe; detection; assay; C.albicans yeast;
XX species specific sequence; ss.
XX
XX Candida albicans.
XX
XX EP595167-Al.
XX
XX 04-MAY-1994.
XX
XX 19-OCT-1993; 93EP-00116865.
XX
XX 30-OCT-1992; 92DE-04236708.
XX
XX (FARB ) BAYER AG.
XX
XX Springer W, Plempel M, Loebberding A;
XX
XX WPI; 1994-145805/18.
XX
XX New hybridisation reagents specific for Candida albicans - are
XX polynucleotide and oligo:nucleotide probes, providing high sensitivity
XX and early diagnosis of infection.
XX
XX Claim 9; Page 33; 44pp; German.
XX
XX A C.albicans gene library was prepared in pBR322 and inserts were
XX selected for multiple presence in the genome, strong conservation without
XX deletions or insertions and absolute specificity for C.albicans. Gene
XX probe 431.19 (AAQ62552) hybridised to all but 4 of the 87 clinical
XX isolates of C.albicans being tested. A clone (436.1) was then isolated
XX from the 4 isolates not recognised by 431.19. Some 100mer
XX oligonucleotides covering the complete sequences of 431.19 and 436.1 were
XX synthesised and tested (see AAQ62558-Q62594). All were found to be
XX absolutely specific for C.albicans. (Updated on 25-MAR-2003 to correct PN
XX field.)
XX
XX Sequence 100 BP; 24 A; 11 C; 29 G; 36 T; 0 U; 0 Other;
XX
XX Query Match 6.1%; Score 76; DB 2; Length 100;
XX Best Local Similarity 85.0%; Pred. No. 2.2e-08;
XX Matches 85; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1019 AAATTTTGCACCTATTTCACCACTACCACTACCACTTCAATGTTGGTGACTACTT 1078
DB 100 AAATTTTGCACCTATTTCACCACTACCACTACCACTTCAATGTTGGTGACTACTT 41

QY 1079 CCTATCTGACTAAGACTGCACCAATTTGTTGAACAGCTAC 1118
DB 40 CCTACAGAACCCAAACTGTACCAATAGACAACTGCTAC 1

RESULT 13
AAQ62592/c
ID AAQ62592 standard; DNA; 100 BP.
XX
AC AAQ62592;
XX
XX 25-MAR-2003 (revised)
DT 07-DEC-1994 (first entry)
XX
XX Candida albicans-specific hybridisation probe.
XX
XX DNA hybridisation probe; detection; assay; C.albicans yeast;
XX species specific sequence; ss.
XX
```

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XX OS Candida albicans.
XX PN EP595167-A1.
XX PD 04-MAY-1994.
XX PF 19-OCT-1993; 93EP-00116865.
XX PR 30-OCT-1992; 92DE-04236708.
XX PA (FARB ) BAYER AG.
XX PI Springer W, Plempel M, Loebberding A;
XX DR WPI; 1994-145805/18.
XX PT New hybridisation reagents specific for Candida albicans - are
XX FT polynucleotide and oligo:nucleotide probes, providing high sensitivity
XX FT and early diagnosis of infection.
XX PS Claim 9; Page 34; 44pp; German.
XX CC A C.albicans gene library was prepared in pBR322 and inserts were
CC CC selected for multiple presence in the genome, strong conservation without
CC CC deletions or insertions and absolute specificity for C.albicans. Gene
CC CC probe 431.19 (AAQ62552) hybridised to all but 4 of the 87 clinical
CC CC isolates of C.albicans being tested. A clone (436.1) was then isolated
CC CC from the 4 isolates not recognised by 431.19. Some 100mer
CC CC oligonucleotides covering the complete sequences of 431.19 and 436.1 were
CC CC synthesised and tested (see AAQ62558-Q62594). All were found to be
CC CC absolutely specific for C.albicans. (Updated on 25-MAR-2003 to correct PN
CC CC field.)
XX SQ Sequence 100 BP; 39 A; 15 C; 19 G; 27 T; 0 U; 0 Other;
Query Match 5.5%; Score 68; DB 2; Length 100;
Best Local Similarity 80.0%; Pred. No. 1.8e-06;
Matches 80; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 719 CATCTAATGAATTCAGATTAATATCAAAATGTAACCTGCTGCTATCGTCCATTATTG 778
DB 100 CATCTAATGTTATCTCTATCATATGAAATATCCCTGCGAGGTATGCTCCATTATTG 41
QY 779 ATGCTTATATTCTGCTACAGATGTTAACCAATATCTTT 818
DB 40 ACGTTTATGATCTGCTCCGAGTGTAAACAGTATATTTT 1
RESULT 14
AAA61847
ID AAA61847 standard; DNA; 5511 BP.
XX AC AAA61847;
XX DT 28-OCT-2000 (first entry)
XX DE Cryptosporidium parvum Iowa isolate GP900 ORF.
XX KW GP900; Iowa isolate; glycoprotein; antibody; cryptosporidiosis;
XX KW competitive inhibition; attachment; invasion; ligand binding; sporozoite;
XX KW merozoite; diarrhoea; protozoa; open reading frame; ORF; ds.
XX OS Cryptosporidium parvum.
XX FH Key Location/Qualifiers
XX FT 1..5511
XX FT CDS /*tag= a
XX FT /product= "Cryptosporidium parvum Iowa isolate GP900"
XX FT /note= "No stop codon given"
XX PN US6071518-A.
XX
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PD 06-JUN-2000.
XX 12-SEP-1997; 97US-00928361.
XX 29-MAY-1992; 92US-00891301.
XX PR 01-JUN-1993; 93US-00071880.
XX PR 03-APR-1995; 95US-00415751.
XX PR 14-AUG-1996; 96US-00700651.
XX PR 13-SEP-1996; 96US-0026062P.
XX (REGC ) UNIV CALIFORNIA.
XX PI Petersen C;
XX WPI; 2000-422065/36.
XX DR P-PSDB; AAB11726.
XX PT New GP900 protein fragments and fusion proteins of Cryptosporidium
XX FT parvum, useful for detecting the presence of the parasite, and diagnosing
XX FT or treating Cryptosporidium infections by competitive inhibition of the
XX FT function of GP900.
XX PS Claim 16; Col 37-42; 59pp; English.
XX CC The invention relates to the GP900 glycoprotein of the protozoan
CC CC Cryptosporidium parvum, DNA encoding it, GP900 fragments, and fusion
CC CC proteins comprising GP900 fragments. The invention also relates to the
CC CC administration of GP900 or fragments thereof to a host to elicit anti-
CC CC GP900 antibody production, and to a method of cryptosporidiosis treatment
CC CC or prophylaxis comprising administration of anti-GP900 antibodies to an
CC CC individual. Cryptosporidium parvum GP900 and GP900 fragments are able to
CC CC competitively inhibit sporozoite or merozoite attachment or invasion, and
CC CC are also useful for the generation of anti-GP900 antibodies. The
CC CC antibodies also inhibit sporozoite or merozoite attachment/invasion and
CC CC additionally inhibit the binding of GP900 ligands to GP900. GP900
CC CC proteins, fragments and antibodies may therefore be used to treat or
CC CC prevent cryptosporidiosis. Infection with Cryptosporidium is a common
CC CC cause of diarrhoea in humans and causes life-threatening diarrhoea in
CC CC immunocompromised persons. Cryptosporidiosis can be contracted from
CC CC contaminated municipal water supplies (e.g., public swimming pools). It
CC CC is also a cause of disease in animals, resulting in financial losses in
CC CC agriculture. GP900 fragments, fusion proteins and antibodies may also be
CC CC used for the diagnosis of Cryptosporidium parvum infections, and for the
CC CC detection of the parasite in the environment. The present sequence
CC CC represents the open erasing frame (ORF) encoding the GP900 protein of the
CC CC Iowa isolate of Cryptosporidium parvum
XX SQ Sequence 5511 BP; 1964 A; 1204 C; 944 G; 1399 T; 0 U; 0 Other;
Query Match 4.9%; Score 61.4; DB 3; Length 5511;
Best Local Similarity 50.9%; Pred. No. 0.00021;
Matches 146; Conservative 0; Mismatches 141; Indels 0; Gaps 0;
QY 933 TGCTACAAGTACAGAGTTACAGACAGTACCACTGCTGCTGCTACTTTTACCATTCAATCC 992
DB 1035 TACTACTACGACAAACAAACAACTACTACTACTACTACTACTACTACTACTACTACTAC 1094
QY 993 AAGTGTGTATATAAACCACAAACAAATCGAAATTTTGCACACCTATTCCACCACTACCATCAC 1052
DB 1095 CACGACAACTACAAACAAACAAACCACTACCAAGAACCAACAAACAAACAAACAAAC 1154
QY 1053 AACTTCATATGTTGGTGTGACTACTTCTCTATCTGATAGACTGACCAATGGTGAAC 1112
DB 1155 AACTACTACTACTACAAACAAACAAACAACTACTACTACTACTACTACTACTACTACTAC 1214
QY 1113 AGTACTGTTATGTTGATGTGCGCATATCATACCAACTGTTTACCACTGAATGGAC 1172
DB 1215 TACTACTACTACTACTACTACCAACCAACCAACCAACCAACCACTACCAAGAACCAAC 1274
QY 1173 AGGAACAATCACTTACCACCAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1219
DB 1275 AACACAAACAAACAAACAAACAACTACTACTACTACTACTACTACTACTACTACTACTAC 1321
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Search completed: March 23, 2005, 10:45:49
Job time : 526 secs

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RESULT 15
ABT04776
ID ABT04776 standard; DNA; 5511 BP.
XX AC
XX ABT04776;
XX DT
XX 27-SEP-2002 (first entry)
XX DE
XX C parvum GP900 gene fragment SEQ ID NO: 2.
XX KW
XX Cryptosporidium detection; GP900; P68; cryptopain; cryptosporidiosis;
XX gene; ds.
XX OS
XX Cryptosporidium parvum.
XX PN
XX WO200194631-A1.
XX PD
XX 13-DEC-2001.
XX PF
XX 14-MAY-2001; 2001WO-US015624.
XX PR
XX 06-JUN-2000; 2000US-0058995.
XX PA
XX (REGC ) UNIV CALIFORNIA.
XX PI
XX Petersen C, Barnes DA, Nelson RG, Gut J;
XX DR
XX WPI; 2002-566447/60.
XX CC
XX Detecting Cryptosporidium in biological and environmental samples and
XX diagnosis of cryptosporidiosis involves, contacting the sample with
XX Cryptosporidium GP900, P68 or cryptopain antigen, antibody, DNA or RNA.
XX PS
XX Disclosure; Page 99-101; 157pp; English.
XX CC
XX The present invention relates to a method of detecting Cryptosporidium in
XX biological and environmental samples, and of diagnosing
XX cryptosporidiosis. This involves obtaining a sample and contacting it
XX with Cryptosporidium GP900, P68 or cryptopain antigen, antibody, DNA or
XX RNA, or its variant, mutant or fragment. The method is also useful for
XX detecting and identifying individual Cryptosporidium isolates based on
XX the genetic characteristics, and for diagnosis of prior or concurrent
XX Cryptosporidium infection. The present sequence is a C. parvum coding
XX sequence used in the exemplification of the invention
XX SQ
XX Sequence 5511 BP; 1964 A; 1204 C; 944 G; 1399 T; 0 U; 0 Other;
XX
XX Query Match 4.9%; Score 61.4; DB 6; Length 5511;
XX Best Local Similarity 50.9%; Pred. No. 0.00021;
XX Matches 146; Conservative 0; Mismatches 141; Indels 0; Gaps 0;
QY 933 TGCTAACTAGAACAGTTACAGACAGTACCACTGCTGCTACTACTTTTACCAATTCATCC 992
DB 1035 TACTACTAGGACACCAACCAACCACTACTACTACTACTACTACTACTACTACTACT 1094
QY 993 AAGTGTGATAAACCAAAACATCGAAATTTTGGCACTTATCCCACTACCAATCCAC 1052
DB 1095 CACGACAACTACCAACCAACCACTACCAAGAAACCAACCAACCAACCAACCAAC 1154
QY 1053 AACTTCATATGTTGGTGTGACTTCTCTATCTGACTAAGACTGCACCCTTTGGTGAAC 1112
DB 1155 AACTTACTACTACTACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 1214
QY 1113 AGCTACTGTTATTTGTTGTCATATCATCTACCACTGTTTACCACTGATGATCC 1172
DB 1215 TACTACTACTACTACTACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 1274
QY 1173 AGGAACATCATCTACCAACCAACCACTGGTACCACTCAACTGATTCAA 1219
DB 1275 AACCAACCAACCAACCAACCAACCACTACTACTACTACTACTACTACTACTACT 1321
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OM nucleic - protein search, using frame_plus_n2p model
Run on: September 8, 2005, 17:41:17 ; Search time 202 Seconds
(without alignments)
4854.553 Million cell updates/sec

Title: US-09-715-876-7_COPY_52_1296
Perfect score: 2297
Sequence: 1 aagacaatcactgtgtttt.....cagtggtggtacaagtcca 1245

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1774312 seqs, 393823214 residues

Total number of hits satisfying chosen parameters: 3548624

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-DB=Published Applications AA -QFMT=fastran -SUFFIX=rapb -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62
-TRANS-human40.cdi -LIST=45 -DOCALLIGN=200 -THR NORM=ext -HEAPSZE=500 -MINLEN=0
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -SCOR=ext -HEAPSZE=500 -MINLEN=0
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA:
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7: /cgm2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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12: /cgm2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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17: /cgm2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgm2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep.*
19: /cgm2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgm2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgm2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgm2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2174	94.6	1260	14	US-10-245-802-8	Sequence 8, Appli
2	1885	82.1	1119	14	US-10-245-802-12	Sequence 12, Appli
3	1865	81.2	1270	14	US-10-245-802-16	Sequence 16, Appli
4	1832	79.8	1047	14	US-10-245-802-22	Sequence 22, Appli
5	1769.5	77.0	468	14	US-10-245-802-10	Sequence 10, Appli
6	1596	69.5	469	14	US-10-245-802-14	Sequence 14, Appli
7	1544.5	67.2	468	14	US-10-245-802-24	Sequence 24, Appli
8	1500	65.3	1443	14	US-10-245-802-18	Sequence 28, Appli
9	961.5	41.9	2297	14	US-10-245-802-20	Sequence 20, Appli
10	308.5	13.4	650	15	US-10-369-493-22177	Sequence 22177, A
11	179	7.8	800	14	US-10-029-386-32198	Sequence 32198, A
12	177	7.7	1322	9	US-09-801-368-114	Sequence 114, App
13	177	7.7	1322	15	US-10-369-493-1353	Sequence 1353, Ap
14	177	7.7	1537	9	US-09-801-368-104	Sequence 104, App
15	177	7.7	1537	15	US-10-369-493-1398	Sequence 1398, Ap
16	177	7.7	1537	17	US-10-324-035-17	Sequence 17, Appli
17	172	7.5	1217	16	US-10-734-564-122	Sequence 122, App
18	170	7.4	957	10	US-09-840-746-19	Sequence 19, Appli
19	165.5	7.2	4262	17	US-10-704-781-4	Sequence 4, Appli
20	165.5	7.2	4493	17	US-10-704-781-3	Sequence 3, Appli
21	161.5	7.0	1075	9	US-09-801-368-110	Sequence 110, Appli
22	161.5	7.0	1075	15	US-10-369-493-22068	Sequence 22068, A
23	156	6.8	688	9	US-09-864-761-36047	Sequence 36047, A
24	154.5	6.7	1367	9	US-09-801-368-108	Sequence 108, App
25	154	6.7	1283	15	US-10-369-493-22616	Sequence 22616, A
26	151.5	6.6	1797	15	US-10-369-493-5176	Sequence 5176, Ap
27	151.5	6.6	1805	15	US-10-369-493-5177	Sequence 5177, Ap
28	150.5	6.6	288	9	US-09-216-393-341	Sequence 341, App
29	150.5	6.6	288	9	US-09-216-393-344	Sequence 344, App
30	150.5	6.6	288	14	US-10-321-856-341	Sequence 341, App
31	150.5	6.6	288	14	US-10-321-856-344	Sequence 344, App
32	150.5	6.6	725	15	US-10-369-493-2004	Sequence 2004, App
33	150	6.5	386	9	US-09-864-761-35720	Sequence 35720, A
34	149.5	6.5	2139	17	US-10-480-456-1	Sequence 1, Appli
35	146.5	6.4	1169	9	US-09-801-368-106	Sequence 106, App
36	146.5	6.4	1169	15	US-10-369-493-22288	Sequence 22288, A
37	146	6.4	951	15	US-10-282-122A-54163	Sequence 54163, A
38	145.5	6.3	1924	17	US-10-831-070-78	Sequence 78, Appli
39	145	6.3	1041	15	US-10-369-493-1935	Sequence 1935, Ap
40	145	6.3	1609	15	US-10-369-493-1535	Sequence 1535, Ap
41	145	6.3	2435	15	US-10-282-122A-47453	Sequence 47453, A
42	144.5	6.3	609	15	US-10-369-493-22725	Sequence 22725, A
43	144.5	6.3	609	15	US-10-369-493-22806	Sequence 22806, A
44	144.5	6.3	3930	15	US-10-282-122A-46817	Sequence 46817, A
45	143	6.2	550	15	US-10-369-493-10236	Sequence 10236, A

ALIGNMENTS

RESULT 1
US-10-245-802-8
; Sequence 8, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 1260
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-245-802-8

Alignment Scores:

Pred. No.: 1,16e-189 Length: 1260
Score: 2174.00 Matches: 413
Percent Similarity: 99.52% Conservative: 0
Best Local Similarity: 99.52% Mismatches: 2
Query Match: 94.65% Indels: 0
DB: 14 Gaps: 0

US-09-715-876-7_COPY_52_1296 (1-1245) x US-10-245-802-8 (1-1260)

QY 1 AAGACATCACTGGTGTGTTTGTAGTAAATCAATTAATCGTCCAAATGCTGCTAAAT 60
DB 18 LysThrIleThrGlyValPheAspSerPheAsnSerLeuThrTrpSerAsnAlaAlaAsn 37
QY 61 TAGCTTTCAAAGGCCAGGATACCCAACTTGGAATGCTGTTTGGTGGTCTTAGAT 120
DB 38 TyrAlaPheLysGlyProGlyTyrProThrTrpAsnAlaValLeuGlyTrpSerLeuAsp 57
QY 121 GGTACCAAGTCCAAATCCAGGGGATACATTCACATTTGAATATGCATGTGTGTTTAAATAT 180
DB 58 GlyThrSerAlaAsnProGlyAspThrPheThrLeuAsnMetProCysValPheLysTyr 77
QY 181 ACTACTTCAAAAACATCTGTTGATTTAACTGCCGATGGTGTAAATATGCTACTGTCAA 240
DB 78 ThrThrSerGlnThrSerValAspLeuThrAlaAspGlyValLysTyrAlaThrCysGln 97
QY 241 TTTTATCTGGTGAAGAATTCACAACTTTTCTACATTAACATGACTGTGGAACGAGCT 300
DB 98 PheTyrSerGlyGluGluPheThrThrPheSerThrLeuThrCysThrValAsnAspAla 117
QY 301 TTGAAATCATCCATTAAAGGATTTGGTACAGTTACTTTTACCAATGTCATTCAATGTTGGT 360
DB 118 LeuLysSerSerIleLysAlaPheGlyThrValThrLeuProIleAlaPheAsnValGly 137
QY 361 GGAACAGGTTTCATCAACTGATTTGGAAAGATTTCAAATGTTTACTGCTGTGTCACCAATACA 420
DB 138 GlyThrGlySerSerThrAspLeuGluAspSerLysCysPheThrAlaGlyThrAsnThr 157
QY 421 GTCATTTAATGATGTGATAAGATATCTCAATGATGTTGAGTTGAAAGTCAACC 480
DB 158 ValThrPheAsnAspGlyAspLysAspIleSerIleAspValGluPheGluLysSerThr 177
QY 481 GTTCATCAAGTGCATATTTGATGCTTCCAGAGTTATGCAAGTCTCAATAAGGTCACA 540
DB 178 ValAspProSerAlaTyrLeuTyrAlaSerArgValMetProSerLeuAsnLysValThr 197
QY 541 ACTCTTTTGTGGCCACCAATGTGAAAATGGTTTACACATCTGTGTAACAATGGGGTCTCC 600
DB 198 ThrLeuPheValAlaProGlnCysGluAsnGlyTyrThrSerGlyThrMetGlyPheSer 217
QY 601 AGTAGTAACGGTGAAGTGTGTTTATGATGCTCAAAATATTCATATGCTATCAACAAGGA 660
DB 218 SerSerAsnGlyAspValAlaIleAspCysSerAsnIleHisIleGlyIleThrLysGly 237
QY 661 TTAATGATGGAATATCCGGTTTCATCTGAATCATTTAGTTACACTAAACCTTGATACA 720
DB 238 LeuAsnAspTrpAsnTyrProValSerSerGluSerPheSerTyrThrLysThrCysThr 257
QY 721 TCTAATGGAATTCAGATTAATATCAAAATGTACCTGCTGGTTATGCTCCATTTATGAT 780
DB 258 SerAsnGlyIleGlnIleLysTyrGlnAsnValProAlaGlyTyrArgProPheIleAsp 277
QY 781 GCTTATATTTCTGACAGATGTTAAACCAATATCTTAGCATATACATGATGATATACT 840
DB 278 AlaTyrIleSerAlaThrAspValAsnGlnTyrThrLeuAlaTyrThrAsnAspTyrThr 297
QY 841 TGCTGTCAGTCTGCTGCAAGTAAACCTTTTCACTTTTAAGATGGAATGGAATCAAGAAT 900
DB 298 CysAlaGlySerArgSerGlnSerLysProPheThrLeuArgTrpThrGlyTyrLysAsn 317
QY 901 AGTCAATGCCGATCTAAACGGTATTTGTCATTTGCTCAACTAGAACAGTTACAGACGT 960

DB 318 SerAspAlaGlySerAsnGlyIleValIleValAlaIaThrThrArgThrValThrAspSer 337
QY 961 ACCACTGCTGTCACTACTTTTACATTCCAATCCAAAGTGTGTGATAAAACCAAAACAAATCGAA 1020
DB 338 ThrThrAlaValThrThrLeuProPheAsnProSerValAspLysThrLysThrIleGlu 357
QY 1021 ATTTTGCACCTATTCCCAACCACTACCATCACAACTTCATATGTTGGTGTGACTACTTCC 1080
DB 358 IleLeuGlnProIleProThrThrIleThrThrSerTyrValGlyValThrThrSer 377
QY 1081 TATCTGACTAAGACTGCACCAATTTGGTGAACAGCTACTGTTATTGTTGATGTCATAT 1140
DB 378 TyrSerThrLysThrAlaProIleGlyGluThrAlaThrValIleValAspValProTyr 397
QY 1141 CATACTACCACAACTGTTTACCAGTGAATGGACAGGAACAATCACTACCACCAACCTCGT 1200
DB 398 HisThrThrThrThrValThrSerGluThrThrGlyThrIleThrThrThrThrArg 417
QY 1201 ACCAATCCAACTGATTCAAATTCACACAGTGGTGTACAAAGTTCCA 1245
DB 418 ThrAsnProThrAspSerIleAspThrValValValGlnValPro 432

RESULT 2
US-10-245-802-12
; Sequence 12, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 1119
; TYPE: PR1
; ORGANISM: Candida albicans
US-10-245-802-12

Alignment Scores:
Pred. No.: 3,07e-163 Length: 1119
Score: 1885.00 Matches: 352
Percent Similarity: 92.05% Conservative: 30
Best Local Similarity: 84.82% Mismatches: 33
Query Match: 82.06% Indels: 0
DB: 14 Gaps: 0

US-09-715-876-7_COPY_52_1296 (1-1245) x US-10-245-802-12 (1-1119)

QY 1 AAGACATCACTGGTGTGTTTGTAGTAAATCAATTAATCGTCCAAATGCTGCTAAAT 60
DB 18 LysThrIleThrGlyValPheAsnSerPheAsnSerLeuThrTrpSerAsnAlaAlaThr 37
QY 61 TAGCTTTCAAAGGCCAGGATACCCAACTTGGAATGCTGTTTGGTGGTCTTAGAT 120
DB 38 TyrAsnTyrLysGlyProGlyThrProThrTrpAsnAlaValLeuGlyTrpSerLeuAsp 57
QY 121 GGTACCAAGTCCAAATCCAGGGGATACATTCACATTTGAATATGCTGCTGTTTAAATAT 180
DB 58 GlyThrSerAlaSerProGlyAspThrPheThrLeuAsnMetProCysValPheLysPhe 77
QY 181 ACTACTTCAAAAACATCTGTTGATTTAACTGCCGATGGTGTGTTAAATATGCTACTGTCAA 240
DB 78 ThrThrSerGlnThrSerValAspLeuThrAlaHisGlyValLysTyrAlaThrCysGln 97
QY 241 TTTTATCTGGTGAAGAATTCACAACTTTTCTACATTAACATGATGCTGTGGAACGAGCT 300
DB 98 PheGlnAlaGlyGluGluPheMetThrPheSerThrLeuThrCysThrValSerAsnThr 117

Db 418 ThrAenProThrAspSerIleAspThrValIleValGlnValPro 432

RESULT 5

US-10-245-802-10

; Sequence 10, Application US/10245802

; Publication No. US20030124134A1

; GENERAL INFORMATION:

; APPLICANT: Edwards, John E.

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST

; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS

; FILE REFERENCE: 013361.4003

; CURRENT APPLICATION NUMBER: US/10/245,802

; CURRENT FILING DATE: 2002-09-13

; PRIOR APPLICATION NUMBER: US 09/715,876

; PRIOR FILING DATE: 2000-11-18

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 10

; LENGTH: 468

; TYPE: PRT

; ORGANISM: Candida albicans

US-10-245-802-10

Alignment Scores:

Pred. No.:	8,72e-153	Length:	468
Score:	1769.50	Matches:	333
Percent Similarity:	86.75%	Conservative:	27
Best Local Similarity:	80.24%	Mismatches:	54
Query Match:	77.04%	Indels:	1
DB:	14	Gaps:	1

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Qy	61	TATGCTTTCAAGGCCAGGATACCCAACTTGGAAATGCTGTTTGGTGGTCTCTAGAT	120
Db	38	TyrAlaIleThrGlyProAsnArgProThrTrpAsnAlaValLeuGlyTrpSerLeuAsp	57
Qy	121	GGTACAGTGCACATCCAGGGGATACATTCACATTTGAATATGCCATGTGTGTTAAATAT	180
Db	58	GlyThrSerAlaAsnProGlyAspThrPheThrLeuAsnMetProCysValPheIleAsp	77
Qy	181	ACTACTTCACAAACATCTGTTGATTAACGCGATGTTTAAATATGCTACTGTCTCA	240
Db	78	IleThrAspGlnThrSerValAspLeuThrAlaGluGlyValLysThrAlaThrCysGln	97
Qy	241	TTTTATTCTGGTGAAGATTCCAACTTTTCTACATTAAACATGACTGTGAACGACGCT	300
Db	98	PheThrSerGlyGluGluPheThrThrPheSerSerLeuLysCysThrValSerAsnThr	117
Qy	301	TTGAATCATCATTAAGCAATTTGCTGACAGTTACTTTTACCAATTCATTCATGCTGCT	360
Db	118	LeuThrSerSerIleLysAlaLeuGlyThrValThrLeuProIleSerPheAsnValGly	137
Qy	361	GGAAACAGTTTCATCACTGATTTGGAAGATTCTAAATGTTTACTGCTGGTACCAATACA	420
Db	138	GlyThrGlySerSerValAspLeuGluSerSerGlnCysPheLysAlaGlyThrAsnThr	157
Qy	421	GTCATATTAAATGATGGTGAATAAGTATCTCAATTTGATGTTGAGTTTGAAAGTCAACC	480
Db	158	ValThrPheAsnAspGlyAspLysLysIleSerIleAspValAspPheGluLysThrAsn	177
Qy	481	GTTGATCCAAAGTGCATATTGTTATGCTTCCAGATTATGCCAAGTCTCAATAAGTCA	540
Db	178	GluAspAlaSerGlyThrPheIleAlaSerArgLeuIleProSerIleAsnLysValSer	197
Qy	541	ACTCTTTTGTGGCCACCAATGTGAAATGTTTACATCTGGTACATATGGGTTCTCC	600
Db	198	IleThrTyrValAlaProGlnCysAlaAsnGlyThrThrSerGlyAlaMetGlyPheIle	217

Qy	601	AGTAGTAACGGTGACGTTGCTATTGATTGCTCAAAATATTCATATTGTTGATCACAAGGA	660
Db	218	ValLeuThrGlyAspThrThrIleAspCysSerAsnValHisValGlyIleThrLysGly	237
Qy	661	TTAAATGATTCGAATATATCGGTTTCATCTGAATCATTTAGTTACACTAAACCTTGACA	720
Db	238	LeuAsnAspTrpAsnPheProValSerSerAspSerLeuSerIleThrCysSer	257
Qy	721	TCTAATCGAATTCAGATTAATAATCAAAATGTACTGCTGCTGTTATCTGCTCAATTTAT	780
Db	258	SerThrGlyIleSerIleThrThrGluAsnValProAlaGlyThrArgProPheAsp	277
Qy	781	GCTTATATTCTGCTACAGATGTTAACCAATATATCTTTAGCATATACCAATGATTACT	840
Db	278	ValTyrThrSerValSerGlyGlnAsnArg---GlnLeuArgTyrThrAsnAspTyrAla	296
Qy	841	TGCTGTCGAGTCTGCTGCAAGTAAACCTTTCATTTAAGATGAGTGGATACAAGAT	900
Db	297	CysValGlySerSerLeuGlnSerLysPheAsnLeuArgLeuArgGlyThrAsnAsn	316
Qy	901	AGTGATCCGGATCTTAACGGTATTGTTCAATGTTGCTTACCACTAGAACAGTTTACAGAC	960
Db	317	SerGluAlaAsnSerAsnGlyPheValIleValAlaThrThrArgThrValThrAspSer	336
Qy	961	ACCACTGCTGCTACTACTTTACCATCAATCCAAAGTGTGTGATAAAACCAAAATCGAA	1020
Db	337	ThrThrAlaValThrThrLeuProPheAsnProSerValAspLysThrLysThrIleGlu	356
Qy	1021	ATTTGCAACTATTCCAAACCACTACCATCACACTTCATATGTTGGTGGTACTTCC	1080
Db	357	IleLeuGlnProIleProThrThrThrIleThrThrSerThrSerValGlyValThrThrSer	376
Qy	1081	TATCTGACTGAAGTCTGACCAATTTGTTGAAACAGTACTGTTATTTGTTGATGTCATAT	1140
Db	377	TyrSerThrLysThrAlaProIleGlyGluThrAlaThrValIleValAspValProTyr	396
Qy	1141	CATACTACCAACTGTTTACAGTGAATGAGACAGAAACAATCATCTACCACCAACTCGT	1200
Db	397	HisThrThrThrValThrValThrSerGluThrThrGlyThrIleThrThrThrThrArg	416
Qy	1201	ACCAATCCAACTGATTCATTAATGACACAGTGGTGGTACAGTTCCA 1245	
Db	417	ThrAsnProThrAspSerIleAspThrValValGlnValPro 431	

RESULT 6

US-10-245-802-14

; Sequence 14, Application US/10245802

; Publication No. US20030124134A1

; GENERAL INFORMATION:

; APPLICANT: Edwards, John E.

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST

; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS

; FILE REFERENCE: 013361.4003

; CURRENT APPLICATION NUMBER: US/10/245,802

; CURRENT FILING DATE: 2002-09-13

; PRIOR APPLICATION NUMBER: US 09/715,876

; PRIOR FILING DATE: 2000-11-18

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 14

; LENGTH: 469

; TYPE: PRT

; ORGANISM: Candida albicans

US-10-245-802-14

Alignment Scores:

Pred. No.:	6,48e-137	Length:	469
Score:	1596.00	Matches:	295
Percent Similarity:	81.20%	Conservative:	42
Best Local Similarity:	71.08%	Mismatches:	78
Query Match:	69.48%	Indels:	0
DB:	14	Gaps:	0

US-09-715-876-7_COPY_52_1296 (1-1245) x US-10-245-802-14 (1-469)

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QY 1 AAGACATCACTGGTGTGTTTGTAGTATTTTAAATTCATTAACTGGTCCCAATGCTGCTAAT 60
Db 18 LysValIleThrGlyValPheAsnSerPheAsnSerLeuThrTrpAlaAsnAlaAlaSer 37
QY 61 TATGCTTTCAAAGGCCAGGATACCCAACTTGGAATGCTGTTTGGGTTGGTCTCTAGAT 120
Db 38 TyrProTyrArgGlyProAlaThrProThrTrpThrAlaValIleGlyTrpSerLeuAsp 57
QY 121 GGTACCAAGTGCATCCAGGGATACATTCACATTTGAATATGCCATGTGTTTAAATAT 180
Db 58 GlyAlaThrAlaSerAlaGlyAspThrPheThrLeuAspMetProCysValPheLysPhe 77
QY 181 ACTACTTCCAAACATCTGTGTTTAACTGCGGATGGTGTAAATATGCTACTTGTCAA 240
Db 78 IleThrAspGlnThrSerIleAspLeuValAlaAspGlyArgThrTyAlaThrCysAsn 97
QY 241 TTTTATTCTGTGTGAAGAATTCACAACTTTTCTACATTAACATGATCTGTGAACAGCT 300
Db 98 LeuAsnSerAlaGluGluPheThrThrPheSerSerValSerCysThrValThrThrThr 117
QY 301 TTGAATATCAATCAAGGATTTGGTACAGTTTACTTTTACCAATGTCATTCATGTTGCT 360
Db 118 MetThrAlaAspThrLysAlaIleGlyThrValThrLeuProPheSerPheSerValGly 137
QY 361 GGAACAGTTCATCACTGATTTGGAAGATTTAAATGTTTACTGCTGTGTACCAATACA 420
Db 138 GlySerGlySerAspValAspLeuAlaAsnSerGlnCysPheThrAlaGlyIleAsnThr 157
QY 421 GTCACTTTAATGATGTGATAAGATATCTCAATTCATGATGTGATGTTGAAAAGTCAAC 480
Db 158 ValThrPheAsnAspGlyAspThrSerIleSerThrThrValAlaAspPheGluLysSerThr 177
QY 481 GTTGATCCAAATGATATTTGTATGCTTCAGAGTTATGCCAAGTCTCAATATAGGTACA 540
Db 178 ValAlaSerSerAspArgIleLeuLeuSerArgIleLeuProSerLeuSerGlnAlaVal 197
QY 541 ACTCTTTTGTGGCACCACATGGAATGTTTACACATCTGTCAATGGAATGGGTTCTCC 600
Db 198 AsnLeuPheLeuProGlnGluCysAlaAsnGlyTyrThrSerGlyThrMetGlyPheSer 217
QY 601 AGTAGTAACGGTGCAGTTGCTATTGATTTGCTCAAATATTCATATGTTGATTCACAAAAG 660
Db 218 ThrAlaGlyThrGlyAlaThrIleAspCysSerThrValHisValGlyIleSerAsnGly 237
QY 661 TTAATGATTTGGAATATTCGGTTTCATCTGAATCATTTAGTTACATTAACACTTGTACA 720
Db 238 LeuAsnAspTrpAsnTyrProIleSerSerGluSerPheSerTyrThrLysThrCysThr 257
QY 721 TCTAATGGAATTCAGATTTAAATATCAAAATGTACTGCTGTTATCGTCCATTTATTGAT 780
Db 258 SerThrSerValLeuValThrPheGlnAsnValProAlaGlyTyrArgProPheValAsp 277
QY 781 GCTTATATTTCTGACAGATGTTTAAACCAATATATCTTTAGCATATACCAATGATTAAT 840
Db 278 AlaTyrIleSerAlaThrArgValSerSerTyrThrMetGlnTyrThrAsnIleTyrAla 297
QY 841 TGCTGTCAGTCTGTCGAAAGTAAACCTTTGACCTTTAGATGGATCGATCAAGATCAAGAT 900
Db 298 CysValGlyAlaAlaSerValAspAspSerPheThrHisThrTrpArgGlyTyrSerAsn 317
QY 901 AGTCATGCCGATCTAACGGTATTGTCAATTTGCTACAACTAGAACAGATTACAGACAGT 960
Db 318 SerGlnAlaGlySerAsnGlyIleThrIleValValThrThrArgThrValThrAspSer 337
QY 961 ACCACTGTGTCATCTTTTACCAATCAATCAAGTGTGTATAAAACCAAAACATCGAA 1020
Db 338 ThrThrAlaValThrThrLeuProPheAsnSerAspThrAspLysThrLysThrIleGlu 357
QY 1021 ATTTTGCACCTATTCACACACTTACCATCAACTTCATATGTTGGTGTGACTCTTCC 1080
Db 358 IleLeuGlnProIleProThrThrThrIleThrThrSerTyrValGlyValThrThrSer 377
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QY 1081 TATCTGACTAAGACTGCACCAATTTGGTGAACAGCTACTGTTATTGTTGATGTCATAT 1140
Db 378 TyrSerThrLysThrAlaProIleGlyGluThrAlaThrValIleValAspValProTyr 397
QY 1141 CATACTACCACTGTTTACCAAGTGAATGACAGGACCAATCACTACCAACCACTCGT 1200
Db 398 HisThrThrThrThrValThrSerGluTrpThrGlyThrIleThrThrThrThrArg 417
QY 1201 ACCAATCCAACTGATTCAATTCACAGTGGTGGTCAAGTTCCA 1245
Db 418 ThrAsnProThrAspSerIleAspThrValValGlnValPro 432
```

RESULT 7

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US-10-245-802-24
; Sequence 24, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-245-802-24
```

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Alignment Scores:
Pred. No.: 3,33e-132 Length: 468
Score: 1544.50 Matches: 291
Percent Similarity: 83.13% Conservative: 54
Best Local Similarity: 70.12% Mismatches: 69
Query Match: 67.24% Indels: 1
DB: 14 Gaps: 1
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US-09-715-876-7_COPY_52_1296 (1-1245) x US-10-245-802-24 (1-468)

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QY 1 AAGACATCACTGGTGTGTTTGTAGTATTTTAAATTCATTAACTGGTCCCAATGCTGCTAAT 60
Db 18 LysThrIleThrGlyValPheAsnSerPheAspSerLeuThrTyrThrArgSerValGlu 37
QY 61 TATGCTTTCAAAGGCCAGGATACCCAACTTGGAATGCTGTTTGGGTTGGTCTCTAGAT 120
Db 38 TyrAlaTyrLysGlyProGluThrProThrTyrAsnAlaValLeuGlyTyrSerLeuAsn 57
QY 121 GGTACCAAGTGCATCCAGGGATACATTCACATTCGAATATGTCATGTGTTTAAATAT 180
Db 58 SerThrThrAlaAspProGlyAspThrPheThrLeuIleLeuProCysValPheLysPhe 77
QY 181 ACTACTTCCAAACATCTGTGTTTAACTGCGGATGGTGTAAATATGATCTACTGTCAC 240
Db 78 IleThrThrGlnThrSerValAspLeuThrAlaAspGlyValSerTyrAlaThrCysAsp 97
QY 241 TTTTATTCTGGTGAAGAATTCACAACTTTTCTACATTAACATGCTACTGTGAACGAGCT 300
Db 98 PheAsnAlaGlyGluGluPheThrThrPheSerSerLeuSerCysThrValAsnSerVal 117
QY 301 TTGAATATCAATCAAGGATTTGGTACAGTTTACTTTTACCAATTCATTCATTTGTTG 360
Db 118 SerValSerTyrAlaArgValSerGlyThrValLysLeuProIleThrPheAsnValGly 137
QY 361 GGAACAGTTCATCACTGATTTGGAAGATTTCTAAATGTTTACTGCTGTGTCACCAATACA 420
Db 138 GlyThrGlySerSerValAspLeuAlaAspSerLysCysPheThrAlaGlyLysAsnThr 157
QY 421 GTCACATTTAATGATGTGATAAGATATCTCAATTCATGTTGATGTTGAAAGTCAACC 480
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Db 158 ValThrPheMetAspGlyAspThrLysIleSerThrValAlaSerPro 177
Qy 481 GTTGATCCAAAGTCAATATTGATGCTCCAGAGTATGCGCAAGTCTCAATAAGGTACA 540
Db 178 ValSerProSerGlyTyrIleThrSerSerArgIleIleProSerLeuAsnLysLeuSer 197
Qy 541 ACTCTTTTGGGACCAACAATGGAATGTTACACATCTGTTGACAAATGGGGTCTCC 600
Db 198 SerLeuPheValValProGlnCysGluAsnGlyTyrThrSerGlyIleMetGlyPheVal 217
Qy 601 AGTAGTAACGGTGAGCTGTATTGATTCCTCAATATTCATATTCATATTCGTTATCA 660
Db 218 AlaSerAsnGly--AlaThrIleAspCysSerAsnValAsnIleGlyIleSerLysGly 236
Qy 661 TTAATGATGGAATATTCGGTTTCATCTGAATCAATTCATTCATCACTAAACCTGTACA 720
Db 237 LeuAsnAspTyrAsnPheProValSerSerGluSerPheSerTyrThrLysThrCysThr 256
Qy 721 TCTAATGGAATTCAGATTAAATATCAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 257 SerThrSerIleThrValGluPheGlnAsnValProAlaGlyTyrArgProPheValAsp 276
Qy 781 GCTTATATCTGCTACAGATGTTAAACCAATATATCTTTAGCATATACCAATGATATAT 840
Db 277 AlaTyrIleSerAlaGluAsnIleAspLysTyrThrLeuThrTyrAlaAsnGluTyrThr 296
Qy 841 TGCTGCTGCGATCGCTGCCAAGTAACCTTTCATCTTAAGTGAAGTGGATACAGAT 900
Db 297 CysGluAsnGlyAsnThrValValAspProPheThrLeuThrTyrTyrGlyTyrLysAsn 316
Qy 901 AGTAGTCCGGATCTAAACGGTATTGTCATGTCACAACTAGAACAGTTTACAGACAGT 960
Db 317 SerGluAlaAspSerAspGlyAspValIleValThrValThrValThrValThrValThr 336
Qy 961 ACCACTGCTGCTACTTACCAATTCATCAATCCAGTGTGTATAAACCACCAATCGAA 1020
Db 337 ThrThrAlaValThrThrLeuProPheAsnProSerValAspLysThrGluThrIleGlu 356
Qy 1021 ATTTGCAACCTATTCCACCACTACCACTACCACTACCACTACCACTACCACTACCACT 1080
Db 357 IleLeuGlnProIleProThrThrIleThrThrSerTyrIleGlyIleSerThrSer 376
Qy 1081 TATCTGATGACATGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
Db 377 TyrGluThrLeuThrGlyThrIleGlyThrAlaThrValIleValAspThrProLys 396
Qy 1141 CATACTACCACTGCTTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
Db 397 HisIleThrAlaThrValThrAsnPheTyrThrGlySerIleThrThrThrThrThr 416
Qy 1201 ACCAATCACTGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1245
Db 417 ThrAsnProThrGlySerIleAspThrValIleValGlnIlePro 431

RESULT 8
US-10-245-802-18
; Sequence 18, Application US/10245802
; Publication NO. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; FILE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 1443
; TYPE: PR
```

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; ORGANISM: Candida albicans
US-10-245-802-18
Alignment Scores: 5.46e-128 Length: 1443
Pred. No.: 1500.00 Matches: 281
Percent Similarity: 81.53% Conservative: 59
Best Local Similarity: 67.39% Mismatches: 75
Query Match: 65.30% Indels: 2
DB: 14 Gaps: 1

US-09-715-876-7_COPY_52_1296 (1-1245) x US-10-245-802-18 (1-1443)
Qy 1 AAGACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
Db 19 LysThrIleSerGlyValPheThrSerPheAsnSerLeuThrTyrThrAsnThrGlyAsn 38
Qy 61 TATGCTTTCAAAAGGCCAGATACCCAACTTGGAACTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 39 TyrProTyrGlyGlyProGlyTyrProThrTyrThrAlaValLeuGlyTyrSerLeuAsp 58
Qy 121 GGTACCACTGCCAATCCAGGCGATACATTCACATTCGAATATGCTGCTGCTGCTGCTGCT 180
Db 59 GlyThrLeuAlaSerProGlyAspThrPheThrLeuValMetProCysValPheLysPhe 78
Qy 181 ACTACTTTCACAAACATCTGTTGATTTAACTGCGCATGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 79 IleThrThrGlnThrSerValAspLeuThrAlaAsnGlyValLysTyrAlaThrCysThr 98
Qy 241 TTTTATCTCGTGAAGAATTCACAACTTTTCTACATTAACATGCTGCTGCTGCTGCTGCTGCT 300
Db 99 PheHisAlaGlyGluAspPheThrThrPheSerSerMetSerCysValValAsnAsnGly 118
Qy 301 TTGAAATCATCCATTAAGGCACTTTGGTACAGTTACTTTTACCAGTTGCTGCTGCTGCTGCT 360
Db 119 LeuSerSerAsnIleArgAlaPheGlyThrValArgLeuProLysPheAsnValGly 138
Qy 361 GGAACAGGTTTCATCAACTGATTTTGGAAAGATTTCTAAATGTTTACTGCTGCTGCTGCTGCT 420
Db 139 GlyThrGlySerSerValAsnIleGlnAspSerLysCysPheThrAlaGlyThrAsnThr 158
Qy 421 GTCACTTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
Db 159 ValThrPheThrAspGlyAspHisLysIleSerThrThrValAsnPheProLysThrPro 178
Qy 481 GTTGATCCAGTGCATATTTGCTGCTTCCAGAGTATGCGCAAGTCTCAATAAGGTACA 540
Db 179 GlnSerSerSerSerLeuValTyrPheAlaArgValIleProSerLeuAspLysLeuSer 198
Qy 541 ACTCTTTTGTGGCACCACCAATGTGAAAGTGTGTTACACATCTGCTGCTGCTGCTGCTGCT 600
Db 199 SerLeuValValAlaSerGlnCysThrAlaGlyTyrAlaSerGlyValLeuGlyPheSer 218
Qy 601 AGTAGTAACGGTGAGCTGTATTGATTCCTCAATATTCATATTCATATTCGTTATCA 660
Db 219 AlaThrLysAspAspValThrIleAspCysSerThrIleHisValGlyIleThrAsnGly 238
Qy 661 TTAATGATGGAATTCGCGTTTCATCTGAATCATTAGTCTACACTTAAACCTGTTTACA 720
Db 239 LeuAsnSerTyrAsnMetProValSerSerGluSerPheSerTyrThrLysThrCysThr 258
Qy 721 TCTAATGGAATTCAGATTAAATATCAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 259 ProAsnSerPheIleIleThrTyrGluAsnValProAlaGlyTyrArgProPheIleAsp 278
Qy 781 GCTTATATTTCTGCTACAGATGTTTAAACCAATATATCTTACATATATACCATATAT 834
Db 279 SerTyrValLysLysSerAlaThrAlaThrAsnGlyPheAsnLeuAsnTyrThrAsnIle 298
Qy 835 TATACTTGTGCTGCGAGTCTGCTGCAAGTAGTAACCTTTCACCTTTAAGATGACGATGAT 894
Db 299 TyrAsnCysMetAspGlyLysLysGlyAsnAspProLeuIleTyrPheTyrThrSerTyr 318
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QY 895 AAGAATAGTATGATCGGATCTAAACGGTATTTGTCATTGTCCTACAACTAGACAGTTTACA 954
DB 319 ThrAsnSerAspAlaGlySerAsnGlyAlaValValValThrThrArgThrValThr 338
QY 955 GACAGTACCACTGCTGTCATCTACTTTTACCATTCAATCAAGTGTGTGATAAACCACAAACA 1014
DB 339 AspSerThrThrAlaIleThrThrLeuProPheAspProThrValAspLysThrLysThr 358
QY 1015 ATCGAAATTTTGCAACCTATTCCCAACCACTACCAATCAACACTTCATATGTTGGTGACCT 1074
DB 359 IleGluValIleGluProIleProThrThrThrIleThrThrSerThrValGlyIleSer 378
QY 1075 ACTTCCTATCTGCTAAAGACTGCACCAATTTGGTGAACAGACTACTGTTATTTGTTGATGTG 1134
DB 379 ThrSerLeuSerThrLysThrAlaThrIleGlyThrAlaThrValValValAspVal 398
QY 1135 CCATATCATCTACACAACTGTTTACCAGTGAATGGACAGAACATCACTACACACACA 1194
DB 399 ProTyrHisThrThrThrIleThrSerIleTyrThrGlySerAlaThrThrSerSer 418
QY 1195 ACTCGTACCAATCAACTGATTCAATTTGACACAGTGGTGTTACAAAGTTTCCA 1245
DB 419 ThrTyrThrAsnProThrAspSerIleAspThrValValGluValPro 435

RESULT 9
US-10-245-802-20
; Sequence 20: Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 2297
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-245-802-20

Alignment Scores:
Pred. No.: 1,14e-78 Length: 2297
Score: 961.50 Matches: 192
Percent Similarity: 63.94% Conservative: 74
Best Local Similarity: 46.15% Mismatches: 149
Query Match: 41.86% Indels: 1
DB: 14 Gaps: 1

US-09-715-876-7_copy_52_1296 (1-1245) x US-10-245-802-20 (1-2297)
QY 1 AAGCAATCACTGGTGTGTTTGTATGATGTTTAAATTCATTAACTTGGTCCCAATGCTGCTAAT 60
DB 19 LysGluValThrGlyValPheAsnGluPheAsnSerLeuIleTyrSerTyrThrTyrArg 38
QY 61 TATGCTTTCAAGGCCAGGATACCCAACTTGGAAATGCTGTTGGGTTGGTCTCTAGAT 120
DB 39 AlaArgTyrGluGluIleSerThrLeuThrAlaAsnAlaGluLeuGluTyrAlaLeuAsp 58
QY 121 GGTACCACTGCAATCCAGGGATACATTCACATTTGAATATGCAATGCTGTTGTTTAAATAT 180
DB 59 GlyThrIleAlaSerProGlyAspThrPheThrLeuValMetProCysValTyrLysPhe 78
QY 181 ACTACTTCACAAACATCTGTTGATTTAACTCCCGATGGTGTATTAATATGCTACTTGTCAA 240
DB 79 MetThrTyrGluThrSerValGluLeuThrAlaAsnSerIleAlaTyrAlaThrCysAsp 98
QY 241 TTTTATCTGTTGGAAGATTCACAACTTTTCTACATTAACATGCTACTGTGAACGACGCT 300
DB 1199 PheAspAlaGlyGluAspThrLysSerPheSerLeuLysCysThrValThrAspGlu 118
QY 301 TTGAATATCATCCATTAAGCATTTTGGTACAGTTTACTTTTACCAATTCATTCATTCATTCATTCAT 360
DB 119 LeuThrGluAspThrSerValPheGlySerValIleLeuProIleAlaPheAsnValGly 138
QY 361 GGAACAGGTTCATCAACTGATTTGGAAGATTCCTAAATGTTTACTCTGCTGGTACCAATACA 420
DB 139 GlySerGlySerLysSerThrIleThrAspSerLysCysPheSerGlyTyrAsnThr 158
QY 421 GTCACATTTTAATGATCGTGCATTAAGATATCTCAATTTGATGTTGAGTTTCAAAAGTCAACC 480
DB 159 ValThrPhePheAspGlyAsnAsnGluLeuSerThrThrAlaAsnPheLeuProArgArg 178
QY 481 GTTGATCCCAAGTCATATTGTTGATGCTTCACAGGTTTATGCGAAGTTTCTCAATAGGTGCACA 540
DB 179 GluLeuAlaPheGlyLeuValValSerGluArgLeuSerMetSerLeuAspThrMetThr 198
QY 541 ACTCTTTTGTGGCCACACCAATGTTGAATGTTTACATCTGGTACATGTTGGGTTCTCC 600
DB 199 AsnPheValMetSerThrProCysPheMetGlyTyrGlnSerGlyLysLeuGlyPheThr 218
QY 601 AGTAGTAAACGGTGACGTTGCTATTGATTGCTCAATATTCATATTCATATTCATATTCATATTCAT 660
DB 219 SerAsnAspAspAspPheGluIleAspCysSerSerIleHisValGlyIleThrAsnGlu 238
QY 661 TTAATGATTGGAATTTATTCCTGCTGTTTCTGATTCATTCATTCATTCATTCATTCATTCATTCAT 720
DB 239 IleAsnAspTyrSerMetProValSerSerValProPheAspHisThrIleArgCysThr 258
QY 721 TCTAATGGAATTCAGATTAATCAAAATGATCACTGCTGGTGGTATCGTCCATTTATATGAT 780
DB 259 SerArgAlaLeuTyrIleGluPheLysThrIleProAlaGlyTyrArgProPheValAsp 278
QY 781 GCTTATATTCTGCTACAGATGTTAACCAATATATCTTTAGCATATACCAATACCAATGATTATACT 840
DB 279 AlaIleValGlnIleProThrThrGluProPheValLysTyrThrAsnGluPheAla 298
QY 841 TGTGCTGGCAGTCTGCTGCAAGTAAACCTTTTACCTTTTAAAGATGGACT---GGATACAAG 897
DB 299 CysValAsnGlyIleTyrThrSerIleProPheThrSerPhePheSerGlnProIleLeu 318
QY 898 AATAGTGATGCCGATCTAACGGTATTTGCTATGTTGCTACAACTAGACAGTTCAGAC 957
DB 319 TyrAspGluAlaLeuAlaIleGlyAlaAspLeuValArgThrThrSerThrValIleGly 338
QY 958 AGTACCACCTGCTGCTCACTACTTTTACCATTCAATCCCAAGTGTTCATAAAACCAAAACAATC 1017
DB 339 SerIleThrArgThrThrThrLeuProPheIleSerArgLeuGluLysThrIleThrIle 358
QY 1018 GAAATTTTGCACACTTATCCAACTACCACTACCACTTCAATTCATATGTTGGTGTGACTACT 1077
DB 359 LeuValLeuGluProIleProThrThrThrValThrThrSerHisHisGlyPheAspThr 378
QY 1078 TCCTATCTGCTAAGACTGCACCAATTTGGTGAACAGCTACTGTTATTTGATGTGCCA 1137
DB 379 TyrTyrTyrThrLysLysAlaThrIleGlyAspThrAlaThrValPheIleAspValPro 398
QY 1138 TATCATCTACCACTACCACTGTTTACCAGTGAATGACAGGAACTACTACTACCAACCAACT 1197
DB 399 GlnHisThrAlaThrThrLeuThrThrTyrTyrGlnGluSerSerThrThrAlaThrThr 418
QY 1198 CGTACCACTACCACTGATTCAATTTGACAGTGGTGTGCAAGTTCCA 1245
DB 419 TyrPheAspAspIleAspLeuValAspThrValIleValLysIlePro 434

RESULT 10
US-10-369-493-22177
; Sequence 22177, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
```

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; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 22177
; LENGTH: 650
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; US-10-369-493-22177

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Alignment Scores:		
Pred. No.:	4,268-19	Length: 650
Score:	308.50	Matches: 116
Percent Similarity:	43.3%	Conservative: 79
Best Local Similarity:	25.78%	Mismatches: 190
Query Match:	13.43%	Indels: 65
DB:	15	Gaps: 20

U.S.-09-715-876-7 COPY 52 1296 (1-1245) X US-10-369-493-22177 (1-650)

QY	25	AGTTTAAATCAATTAACTTGGTCCAAAT	-----GCTGCTAATTATGCT	56
Db	21	AsnIleAsnAspIleThrPheSerAsnLeuGluIleThrProLeuThrAlaAsn	-----	38
QY	67	TTCAAGAGGCCAGGATACCACTTGGAAATCTGTTTGGGTGCTCTTA	---GATGGT	123
Db	39	---LysGlnProAsp---GlnGlyTrpThrAlaThrPheAspPheSerIleAlaAspAla	56	
QY	124	ACCAGTGCCAAATCCAGGGGATACATTCACATTTGAATATGCCATGTGTGTTTAAA	-----	177
Db	57	SerSerIleArgGluGlyAspGluPheThrLeuSerMetProHisValTyrArgIleLys	76	
QY	178	---TATACTACTTCACAAACATCTGTTGATTTAACTGCCGATGTGTAAATATGCTACT	234	
Db	77	LeuLeuAsnSerSerGlnThrAlaThrIleSerLeuAlaAspGlyThrGluAlaPheLys	96	
QY	235	TGTCAATTTTATCTGGTGAA	-----GAATTCACAACTTTTCTACATTA	279
Db	97	Cys---TyrValSerGlnGlnAlaAlaTyrLeuTyrGluAsnThrThrPhe	-----	112
QY	280	ACATGTACTGTGAACACGCTTTTGAATCATCCATTAAGGCATTTGGTACAGTTACTTTA	339	
Db	113	ThrCysThrAlaGlnAsnAspLeuSerSerTyrAsnThrIleAspGlySerIleThrPhe	132	
QY	340	CAAATTGCATTCATGTTGGTGGACACAGTTTCATCACTGATTTGGAGATTCTTAATGT	399	
Db	133	SerLeuAsnPheSerAspGlyGlySerTyrGluTyrGluLeuGluAsnAlaLysPhe	152	
QY	400	TTTACTGCTGTGACCAATACAGTCACATTTAATGATGGTGTGATAAGATATCTCAATTTGAT	459	
Db	153	PheLysSerGlyProMetLeuValLysLeuGlyAsnGlnMetSerAspVal	-----	169
QY	460	GTTGAGTTTGAAGTCACACCGTTGATCCAGTGCATAT	-----TTGTATGCTTCC	510
Db	170	ValAsnPhe-----AspProAlaAlaPheThrGluAsnValPheHisSer	184	
QY	511	AGAGTTATGCCAGTCTCAATAAGGTCACACTCTTTTGTGGCACCACCATGTGAAAT	570	
Db	185	GlyArgSerThrGlyTyrGlySerPheGluSerTyrHisLeuGlyMetTyrCysProAsn	204	
QY	571	GGTTACACATCTCGT	-----ACAATGGGGTTCTCCAGTAGTAAACGGTACGTTGCT	621
Db	205	GlyTyrPheLeuGlyGlyThrGluLysIleAspTyrAspSerSerAsnAsnValAsp	224	
QY	622	ATTGATTGCTCAAATATTTCATATTGGTATCATCAAAAAGGATTAAATGATTTGGAAATTCGG	681	

RESULT 11

US-10-029-386-32198
; Sequence 32198, Application US/10029386
; Publication No. US20030194704A1

; PUBLICATION NO. US20
: GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

: AFFILIANT: KANZ, DAVID K.
: APPLICANT: HANZEL, DAVID K.

: TITLE OF INVENTION: HUMAN GENOME-DERIVED SIN

TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

FILE REFERENCE: AEOMICA-X-2

; CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

; SOFTWARE: Anno

; SEQ ID NO 321

; LENGTH: 8

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; TYPE: PRT

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ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO AC007663.28

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.6

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.2

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.3

; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.3

; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9

; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3

; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

Db GluGlnProProlleThrSerThrAsnPhethrileAsn-----Glyile 193
Qy 316 AAGCAATT-----GGTACAGTT----- 333
Db LysProTrpAengGlySerProProAsnIleThrGlyThrValTyrMetTyrAlaGly 213
Qy 334 -----ACTTTACCAATT 345
Db 214 PheTyrTyrProMetLysIleValTyrSerAsnAlaValAlaTrpGlyThrLeuProile 233
Qy 346 GCATTCAATGTT---GGTGGACAGGTTTCATCACTGATTGGAGAGATTCTAAATGTTTT 402
Db 234 SerValThrLeuProAspGlyThrThrValSerAspPheGluGly----- 249
Qy 403 ACTGCTGTACCAATACAGTCACATTTAATCATGGTGTATAAGATATCTCAATTGATTT 462
Db 250 -----TyrValTyrThrPhe-----AspAsnAsnLeuSer----- 259
Qy 463 GAGTTTGAAGAGTCAACGGTTGATCCAGTGCATATTTGTTATGCTTCCAGAGTTATGCCA 522
Db 260 GlnProAsnCysThrIleProAspProSerAsnTyrThr-----ValSerThrThrIleThr 278
Qy 523 AGTCTCAATAAGGTCACAACTCTTTTGTGTGGCACCAACAATGTGAATGGTTACACATCT 582
Db 279 ThrThrGluProTrpThrGlyThrPheThrSerThrSerThrGluMetThrThrValThr 298
Qy 583 GGTACAATGGGTTCTCAGTAGTAACCGTGACGTTGCTATTGATTGCTCAAAATTCAT 642
Db 299 GlyThrAsnGlyValProThrAspGluThrValIleValIleArgThrProThrThrAla 318
Qy 643 ATTGGTATCACAAAGGATTAAATGATTGAATTATCCGTTTCATCTGAATCATTTAGT 702
Db 319 SerThrIleThrThrGluProTrpAsnSerThrPheThrSerThrSerThrGlu 338
Qy 703 TACATAAACTGTGTACATCTAATGGAATTCAGATTAATATCAAAATGTACCTGCTGT 762
Db 339 LeuthrThrValThrGlyThrAsnGlyValargThrAspGluThrIleIle----- 355
Qy 763 TATGCTCATTTATTGATGCTTATATTTCTGTCAGATGTTAACCATAATATCTTTAGCA 822
Db 356 -----ValIleArgThrProThrThrAlaThrThrAlaIleThrThrGluPro 372
Qy 823 TATACCAATGATTACTGTGCTGGCAGTGTCTGCAAGTAAAGTAAACCTTTCACTTTAAGA 882
Db 373 TrpAsnSerThrPheThrSerThrSerThrGluLeu----- 384
Qy 883 TGGACTGTGATCAAGATAGTGCAGCGGATCTAACGGTATT-----GTCATTGTT 933
Db 385 -----ThrThrValThrGlyThrAsnGlyLeuProThrAspGluThrile 399
Qy 934 GCTACAAC TAGAAGTTACAGACAGTACCACTGCTGTCTACTTTTA-----CCATTCAT 990
Db 400 IleValIleArgThrProThrThrAlaThrThrAlaMetThrThrGlnProTrpAsn 419
Qy 991 CCAAGTGTGTATAAACCAACA----- 1014
Db 420 AspThrPheThrSerThrSerThrGluLeuThrThrValThrGlyThrAsnGlyLeuPro 439
Qy 1015 -----ATCGAATTTTGCACCTATTCCAACCACTATCCACACTACCATCACAACT--- 1056
Db 440 ThrAspGluThrIleIleValIleargThrProThrThrAlaThrThrAlaMetThrThr 459
Qy 1057 -----TCATANGTGGTGTGACTACTTCTCTATCTGACTAAGATGCA 1098
Db 460 ThrGlnProTrpAsnAspThrPheThrSerThrSerThrGluLeuThrThrValThrGly 479
Qy 1099 -----CCATTTGGTGAACAGTACTGTTATTGTTGATGTGCTCATATCACT 1146
Db 480 ThrAsnGlyLeuProThrAspGluThr-----IleIleValIleArgThrProThrThrAla 498
Qy 1147 ACCACA-----ACTGTTACCAAGTGAATGGACGAGCAACAATCACT----- 1185
Db 499 ThrThrAlaMetThrThrGlnProTrpAsnAspThrPheThrSerThrSerThrGlu 518

Qy 1186 ---ACCACCAAACTCGTACCAAT-----CCAATGATTCAATTGACACAGTGGTGTGA 1236
Db 519 IleThrThrValThrGlyThrAsnGlyLeuProThrAsp-----GluThrIleIleVal 536
RESULT 13
US-10-369-493-1353
; Sequence 1353, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 1353
; LENGTH: 1322
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-1353
Alignment Scores:
Pred. No.: 5,61e-07 Length: 1322
Score: 177.00 Matches: 112
Percent Similarity: 34.38% Conservative: 53
Best Local Similarity: 23.33% Mismatches: 181
Query Match: 7.71% Indels: 134
DB: 15 Gaps: 26
US-09-715-876-7_COPY_52_1296 (1-1245) x US-10-369-493-1353 (1-1322)

Qy 58 AATTATGCTTTCAAGGCCAGGATACCCAACTTGGATGCTGTTTGGGT---TGGTCC 114
Db 104 AsnTrpGlyCysLysGlyIleGlyAlaCysSerAsnAsnProIleIleAlaTyrTrpSer 123
Qy 115 TTAGAT-----GTACCAGTGCACATCCAGGGATACATTCACATTGAATATG----- 162
Db 124 ThrAspLeuPheGlyPheTyrThrThrProThrAsnVal---ThrLeuGluMetThrGly 142
Qy 163 -----CCATGTGTGTTAAATATATATATCTCTCACAACATCT 198
Db 143 TyrPheLeuProGlnThrGlySerTyrThrPheLysPheAlaThrValAspAspSer 162
Qy 199 GTTGATTAACTGCCGATGTT---GTTAAATATGCTACTTGTCAATTTTATTCTGGTGAA 255
Db 163 AlaIleLeuSerValGlyGlySerIleAlaPheGluCysCys-----AlaGln 178
Qy 256 GAATTCACAACCTTTTTCATATTAAACATGCTGTGAACGACGCTTTGAAATCATCATCT 315
Db 179 GluGlnProProlleThrSerThrAsnPhethrileAsn-----Glyile 193
Qy 316 AAGCAATT-----GGTACAGTT----- 333
Db 194 LysProTrpAengGlySerProProAsnIleThrGlyThrValTyrMetTyrAlaGly 213
Qy 334 -----ACTTTACCAATT 345
Db 214 PheTyrTyrProMetLysIleValTyrSerAsnAlaValAlaTrpGlyThrLeuProile 233
Qy 346 GCATTCAATGTT---GGTGGACAGGTTTCATCACTGATTGGAGAGATTCTAAATGTTTT 402
Db 234 SerValThrLeuProAspGlyThrThrValSerAspPheGluGly----- 249
Qy 403 ACTGCTGTGTACCAATACAGTCACATTTAATGATGATGATATCTCAATTGATGTT 462

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Db 250 -----TyrValTyrThrPhe-----AspAsnAsnLeuSer----- 259
Qy 463 GAGTTTGAAAGCAACCGTTGATCCAAAGTGCATATTTGTATGCTTCCAGAGTTATGCGCA 522
Db 260 GlnProAsnCysThrIleProAspProSerAsnTyrThr---ValSerThrThrIleThr 278
Qy 523 AGTCTCAATAAGGTCACAACTCTTTTGTGGCCACCAAAATGCGAATGGTATACATCT 582
Db 279 ThrThrGluProThrThrGlyThrPheThrSerThrGluMetThrThrValThr 298
Qy 583 GGTACAAATGGGTTCTCCAGTAGTAACGGTAGCGTGTGCTATTCATTCATTCATTCAT 642
Db 299 GlyThrAsnGlyValProThrAspGluThrValIleValIleArgThrProThrThrAla 318
Qy 643 ATTGGTATCACAAAGGATTAAATGATGGAATTCCTCGGTTTCATCTGAATCATTTAGT 702
Db 319 SerThrIleIleThrThrGluProThrPheThrSerThrPheThrSerThrThrGlu 338
Qy 703 TACACTAAAACTTGTACATCTAATGGAATTCAGATTAAATATCAAAATGACCTGTGGT 762
Db 339 LeuThrThrValThrGlyThrAsnGlyValArgThrAspGluThrIleIle----- 355
Qy 763 TATCGTCCATTATGATGCTATATATTCCTGCTACAGATGTTAACCAATATATCTTAGCA 822
Db 356 -----ValIleArgThrProThrThrAlaThrThrAlaIleThrThrThrGluPro 372
Qy 823 TATACCAATGATATATCTGCTGCGGAGCGCTGCAAAAGTAAACCTTCACTTTAAGA 882
Db 373 TrpAsnSerThrPheThrSerThrSerThrGluLeu----- 384
Qy 883 TGGACTGGATACAGAATAGTAGTCCGCGATCTAAACGGTATT-----GTCATGTT 933
Db 385 -----ThrThrValThrGlyThrAsnGlyLeuProThrAspGluThrIle 399
Qy 934 GCTACAACTAGACAGTTACAGACGATACACCTGCTGCTCACTACTTA-----CAATTCAT 990
Db 400 IleValIleArgThrProThrThrAlaThrThrAlaMetThrThrGlnProThrPsn 419
Qy 991 CCAAGTGTGTAACCAACCAACA----- 1014
Db 420 AspThrPheThrSerThrSerThrGluLeuThrThrValThrGlyThrAsnGlyLeuPro 439
Qy 1015 -----ATCGAAATTTGCAACCTATTCCAAACCACTACCACTACCACT--- 1056
Db 440 ThrAspGluThrIleIleValIleArgThrProThrThrAlaThrThrAlaMetThrThr 459
Qy 1057 -----TCATATGTTGGTGTGACTACTTCTCTATCTGACTAAGACTGCA 1098
Db 460 ThrGlnProThrPsnAspThrPheThrSerThrSerThrGluLeuThrThrValThrGly 479
Qy 1099 -----CCAATTGGTGAACACAGCTACTGTTATTTGATGTCCTATCATCACT 1146
Db 480 ThrAsnGlyLeuProThrAspGluThr-----IleIleValIleArgThrProThrThrAla 498
Qy 1147 ACCACA-----ACTGTTACAGTGAATGGACAGAAACAATCACT----- 1185
Db 499 ThrThrAlaMetThrThrThrGlnProThrPsnAspThrPheThrSerThrSerThrGlu 518
Qy 1186 ---ACCACCACTCGTACCAAT-----CCAACTGATTCATTTGACAGTGGTGTA 1236
Db 519 IleThrThrValThrGlyThrAsnGlyLeuProThrAsp-----GluThrIleIleVal 536
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RESULT 14

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US-09-801-368-104
; Sequence 104, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
```

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; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801.368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 104
; LENGTH: 1537
; TYPE: PRF
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-104
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Alignment Scores:
Pred. No.: 5,86e-07 Length: 1537
Score: 177.00 Matches: 112
Percent Similarity: 32.72% Conservative: 47
Best Local Similarity: 23.05% Mismatches: 181
Query Match: 7,71% Indels: 146
DB: 25
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US-09-715-876-7_COPY_52_1296 (1-1245) x US-09-801-368-104 (1-1537)

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Qy 58 AATTATGCTTCAAGGGCCAGGA---TACCCCACTTGAATGCTGTTTGGGTTGGTCC 114
Db 104 AsnTrpGlyCysIleGlyMetGlyAlaCysSerAsnSerGlnGlyIleAlaTyrTrpSer 123
Qy 115 TTAGAT-----GGTACCAGTCCCAATCCAGGGGATACATTACATTGAATATG--- 162
Db 124 ThrAspLeuPheGlyPheTyrThrProThrAsnVal---ThrLeuGluMetThrGly 142
Qy 163 -----CCATGTGTGTTTAAATATATATCTACTTTCACAA----- 192
Db 143 TyrPheLeuProGlnThrGlySerTyrThrPheLysPheAlaThrValAspAspSer 162
Qy 192 ----- 192
Db 163 AlaIleLeuSerValGlyGlyAlaThrAlaPheAsnCysCysAlaGlnGlnProPro 182
Qy 193 ---ACATCTGTTGATTAACTCCCGATGTGTAA-- 225
Db 183 IleThrSerThrAsnPheThrIleAspGlyIleLysProTrpGlyGlySerLeuProPro 202
Qy 226 -----TATGCTACTGTCAATTTTATTTCTGTGTGAAGAATTCACAACCTTTTCTACATTA 279
Db 203 AsnIleGluGlyThrValTyrMetTyrAlaGlyTyrTyrTyrProMet----- 218
Qy 280 ACATGTACTGTGAACGACGCTTTGAAATCATCATTAAGGCATTTGGTACA----- 330
Db 219 -----LysValValTyrSerAsnAlaValSerTrpGlyThrLeuProIle 233
Qy 331 ---GTTACTTTACAAATTCATTCATTTGTTGGTGAACAGGTTCATCACTGATTTGGAA 387
Db 234 SerValThrLeuPro-----AspGlyThrThrValSerAspAspPheGlu 248
Qy 388 GATTCTAAATGTTTACTGCTGTGTACCAATACATGTCATATTAATGATGTTGATAAAGAT 447
Db 249 Gly-----TyrValTyrSerPheAspAsp----- 256
Qy 448 ATCTCAATTGATGTTGAGTTTGAAGAGTCAACCGTT---GATCCAAAGTGCATTTGTAT 504
Db 257 -----AspLeuSerGlnSerAsnCysThrValProAspProSerAsnTyrAla--- 272
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QY 505 GCTTCCAGAGTTATGCCAAGTCTCAATAAGGTCACAACTCTTTTGGGCACCAACAATGT 564
Db 273 ValSerThrThrThrThrThrGluProThrPheThrSerThrSerThr 292
QY 565 GAAATGGTTACACATCGGTACCAATGGGGTTCCAGTAGTAACGGTGGCTATT 624
Db 293 GluMetThrThrValThrGlyThrAsnGlyValProThrAspGluThrValIleValIle 312
QY 625 GATTGCTCAATATTCATATGGTATCACAAGAGGTTAAATGATTGGAATTCACCGTT 684
Db 313 ArgThrProThrThrAlaSerThrIleThrThrThrGluProThrPasnSerThrPhe 332
QY 685 TCATCTGAATCAATTTAGTTACACTAAACCTTGATCATCTAATGAATTCAGATTAAATAT 744
Db 333 ThrSerThrSerThrGluLeuThrThrValThrGlyThrAsnGlyValArgThrAspGlu 352
QY 745 CAAATGACCTGCTGGTTATCGTCCATTTATGATGCTTATATTTCTGCTACAGATTT 804
Db 353 ThrIleIle-----ValIleArgThrProThrThrAlaThrThrAla 366
QY 805 AACCAATATCTTAGCATATACCAATGATTATCTTGTGCTGGCAGTCGTCGCAAGT 864
Db 367 IleThrThrThrGluProThrPasnSerThrPheThrSerThrSerThrGluLeu----- 384
QY 865 AAACCTTTCACTTTAAGATGACTGATACCAAGATAGTATGATGCGGATCTAAACGGTATT 924
Db 385 -----ThrThrValThrGlyThrAsnGlyLeu 393
QY 925 -----GTCATTGTGTACAACTAGACAGTTACAGACAGTACCACTGCTGCTACT 975
Db 394 ProThrAspGluThrIleIleValIleArgThrProThrThrAlaThrThrAlaMetThr 413
QY 976 ACTTTA-----CCATTCAATCCAGTGTGATAAACCACAAACA----- 1014
Db 414 ThrThrGlnProThrPasnAspThrPheThrSerThrSerThrGluLeuThrThrValThr 433
QY 1015 -----ATCGAAATTTTGCACCTATTCCAAACC 1041
Db 434 GlyThrAsnGlyLeuProThrAspGluThrIleIleValIleArgThrProThrThrAla 453
QY 1042 ACTACCATCACAACT-----TCATATGTTGGTGGTCACTACTTCC 1080
Db 454 ThrThrAlaMetThrThrThrGlnProThrPasnAspThrPheThrSerThrSerThrGlu 473
QY 1081 TATCTGACTAGACTGCA-----CCAAATGTTGTAACAGCTACTGTTATTGTT 1128
Db 474 LeuThrThrValThrGlyThrAsnGlyLeuProThrAspGluThr-----IleIleValIle 492
QY 1129 GATGTGCCATATCATATACACACA-----ACTGTTACAGTGAATGACAGCAACATC 1182
Db 493 ArgThrProThrThrAlaThrThrAlaMetThrThrThrGlnProThrPasnAspThrPhe 512
QY 1183 ACT-----ACCACCAACTCGTACCAAT-----CCAACTGATTCA 1218
Db 513 ThrSerThrSerThrGluIleThrThrValThrGlyThrAsnGlyLeuProThrAsp----- 531
QY 1219 ATTGACACAGTGGTGTA 1236
Db 532 ---GluThrIleIleVal 536

RESULT 15
US-10-369-493-1398
; Sequence 1398, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 1398
; LENGTH: 1537
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-1398
Alignment Scores:
Pred. No.: 5,86e-07 Length: 1537
Score: 177.00 Matches: 112
Percent Similarity: 32.72% Conservative: 47
Best Local Similarity: 23.05% Mismatches: 181
Query Match: 7.71% Indels: 146
DB: 15 Gaps: 25

US-09-715-876-7 copy_52_1296 (1-1245) x US-10-369-493-1398 (1-1537)
QY 58 AATTATGCTTTCAAAGGCCACGGA---TACCRAACTTTGGAATGCTGTTTGGTGTGTC 114
Db 104 AsnTrpGlyCysLysGlyMetGlyAlaCysSerAsnSerGlnGlyIleAlaIleAlaIle 123
QY 115 TTAGAT-----GGTACCAGTCCCAATCCAGGGGATACATTTCACATTGAATATG- 162
Db 124 ThrAspLeuPheGlyPheThrThrProThrAsnVal---ThrLeuGluMetThrGly 142
QY 163 -----CCATGTTGTTTAAATATATCTACTTCCAA- 192
Db 143 TyrPheLeuProProGlnThrGlySerThrPheLysPheAlaThrValAspAspSer 162
QY 192 ----- 192
Db 163 AlaIleLeuSerValGlyGlyAlaThrAlaPheAsnCysCysAlaGlnGlnProPro 182
QY 193 ---ACATCTGTGATTTAACTGCCGATGGTGTAA- 225
Db 183 IleThrSerThrAsnPheThrIleAspGlyIleLysProTrpGlyGlySerLeuProPro 202
QY 226 -----TATGCTACTGTCATTTTATTCGTGTGAGAAATTCACACTTTTCTACATTA 279
Db 203 AsnIleGluGlyThrValTyrMetTyrAlaGlyTyrTyrProMet----- 218
QY 280 ACATGCTGTGAACGACGCTTTCGAATCATCCATTAAGGCATTTGGTACA- 330
Db 219 -----LysValValTyrSerAsnAlaValSerTrpGlyThrLeuProIle 233
QY 331 ---GTTACTTTTACCAATTTGCATTCATTTGGTGGAAACAGGTTTCATCACTGATTGAA 387
Db 234 SerValThrLeuPro-----AspGlyThrThrValSerAspAspPheGlu 248
QY 388 GATTCTAAATGTTTACTGCTGGTACCAATACATCACTGATCACTTAATGATGGTGAATAAGAT 447
Db 249 Gly-----TyrValTyrSerPheAspAsp----- 256
QY 448 ATCTCAATTCATGTTGAGTTTGAAGTCAACCGTT---GATCCAAGTGCATATTTGTAT 504
Db 257 -----AspLeuSerGlnSerAsnCysThrValProAspProSerAsnTyrAla--- 272
QY 505 GCTTCCAGAGTTATGCCAAGTCTCAATAAGGTCACAACTCTTTTGGGCACCAACAATGT 564
Db 273 ValSerThrThrThrThrThrGluProThrPheThrSerThrSerThr 292
QY 565 GAAATGGTTACACATCTGTTACCAATGGGGTTCTCCAGTAGTAACGGTGGCTGCTATT 624
Db 293 GluMetThrThrValThrGlyThrAsnGlyValProThrAspGluThrValIleValIle 312
QY 625 GATTGCTCAATATTCATATGGTATCACAAGAGGTTAAATGATTGGAATTCACCGTT 684
Db 313 ArgThrProThrThrAlaSerThrIleThrThrThrGluProThrPasnSerThrPhe 332

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Qy 685 TCATCTGAATCAATTAGTTACACTAAACCTTGATACATCTAATGGAATTCAGATTAAATAT 744
Db   ::||| ||| ||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
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Db   ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Qy 745 CAAATGTACTGCTGCTTATCGCTCCATTTATTGATGCTTATATTTCTGCTACAGATGTT 804
Db   ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Qy 353 ThrIleIle-----ValIleArgThrProThrAlaThrThrAla 366
Db   ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Qy 805 AACCAATATACCTTTAGCATATACCAATGATTATATCTGTGCTGGCAGTCGTCTGCAAGT 864
Db   ||| ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Qy 367 IleThrThrThrGluProTrpAsnSerThrPheThrSerThrSerThrGluLeu----- 384
Db   ||| ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Qy 865 AAACCTTTCACTTTAAGATGGATGCGATACAGAATAGTATGATCGCGATCTAACGGTATT 924
Db   ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Qy 385 -----ThrThrValThrGlyThrAsnGlyLeu 393
Db   ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Qy 925 -----GTCATGTTGTGTACAACTAGACAGTGTACAGACAGTACCACTGCTGTCACCT 975
Db   ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Qy 394 ProThrAspGluThrIleValIleValIleValIleValIleValIleValIleValIle 413
Db   ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Qy 976 ACTTTA---CCATTCATCCAGTGTGATAAACCAAAACA----- 1014
Db   ||| ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Qy 414 ThrThrGlnProTrpAsnAspThrPheThrSerThrSerThrGluLeuThrThrValThr 433
Db   ||| ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Qy 1015 -----ATCGAAATTTTGCAACCTATTCCAAACC 1041
Db   ||| ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Qy 434 GlyThrAsnGlyLeuProThrAspGluThrIleIleValIleValIleValIleValIle 453
Db   ||| ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Qy 1042 ACTACCATCAAACT-----TCATATGTTGGTGTGACTACTTCC 1080
Db   ||| ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Qy 454 ThrThrAlaMetThrThrGlnProTrpAsnAspThrPheThrSerThrSerThrGlu 473
Db   ||| ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Qy 1081 TATCTGACTAAGACTGCA-----CCATTTGGTGAACAGCTACTGTTATTGTT 1128
Db   ||| ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Qy 474 LeuThrThrValThrGlyThrAsnGlyLeuProThrAspGluThr-----IleIleValIle 492
Db   ||| ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Qy 1129 GATGTGCATATCATCTACACACA-----ACTGTTACCAAGTGAATGGACAGGAACAATC 1182
Db   ||| ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Qy 493 ArgThrProThrThrAlaThrThrAlaMetThrThrGlnProTrpAsnAspThrPhe 512
Db   ||| ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Qy 1183 ACT-----ACCACCACTGCTACCAAT-----CCAAGTGAATCA 1218
Db   ||| ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Qy 513 ThrSerThrSerThrGluIleThrValThrGlyThrAsnGlyLeuProThrAsp--- 531
Db   ||| ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Qy 1219 ATTGACACAGTGGTGTA 1236
Db   ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Qy 532 ---GluThrIleIleVal 536
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Search completed: September 8, 2005, 18:17:05

Job time : 237 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame plus n2p model

Run on: September 8, 2005, 17:29:26 ; Search time 43.5 Seconds
(without alignments)

Title: US-09-715-876-7 COPY 52 1296

perfect score: 1245
Sequence: 1 aagacaatcactcgtgtttt.....cagtgggtacagttcca 1245

Scoring table: BLOSUM62

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Percent	Xgapop	10.0,	Xgapext	0.5
	Ygapop	10.0,	Ygapext	0.5
	Fgapop	6.0,	Fgapext	7.0
	Delop	6.0,	Delxt	7.0

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0

Maximum DB seq length: 200

Post-processing: Minimum

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-MODEL=frame_n2p.model -DEV=xlp
-Q=/Cgna2.1/USPTO.spool_p/US09175876/runat_08092005.172228.18516/app_query.fasta_1.1415
-D=Issued Patents AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCI=0
-BB=1 -START=1 -END=-1 -WATRIX=bloem62 -TRANS=human40_cdi
-LOOPTXT=0 -UNITS=bits -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-LIST=65 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -MINLEN=0 -MAXLEN=2000000000
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09175876 @CGN_1.1.46 @runat_08092005.172228.18516 -NCPU=6 -ICPU=3
-NO MMAP -LARGEXQUERY -NEG SCORE=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIME=0 -5 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6
-DEBFRMT=7 -VCADOP=10 -VCADPT=0 -5 -DETOP=6 -DEEXT=7

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Database :

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Database :
Issued Patents AA:*
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2: /csm2_6/ptodata/1/iaa/5B_COMB pep.*
3: /csm2_6/ptodata/1/iaa/6A_COMB pep.*
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5: /csm2_6/ptodata/1/iaa/PTCTUS COMB pep.*
6: /csm2_6/ptodata/1/iaa/backfile1 pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2170	94.5	1191	4	US-09-248-796A-16243	Sequence 16243, A
2	1899	82.7	780	4	US-09-248-796A-16702	Sequence 16702, A
3	1599	69.6	511	4	US-09-248-796A-14125	Sequence 14125, A
4	1545	67.3	646	4	US-09-248-796A-16701	Sequence 16701, A
5	1365	59.4	1060	4	US-09-248-796A-14123	Sequence 14123, A
6	992.5	43.2	300	4	US-09-248-796A-16245	Sequence 16245, A
7	994.5	42.9	812	4	US-09-248-796A-16244	Sequence 16244, A
8	814	35.4	239	4	US-09-248-796A-16698	Sequence 16698, A
9	594	25.9	232	4	US-09-248-796A-14122	Sequence 14122, A
10	583	25.4	154	4	US-09-248-796A-14119	Sequence 14119, A
11	308.5	13.4	650	3	US-08-362-525-2	Sequence 2, App11
12	239.5	10.7	97	4	US-09-248-796A-23586	Sequence 23586, A

13	192.5	8.4	501	4	US-09-248-796A-14118	Sequence 14118, A
14	189.5	8.2	356	4	US-09-248-796A-14126	Sequence 14126, A
15	177	7.7	1837	1	US-08-325-267A-2	Sequence 2, Appl
16	175.5	7.6	1837	3	US-08-928-361B-5	Sequence 5, Appl
17	175.5	7.6	1837	4	US-09-588-995A-5	Sequence 5, Appl
18	175	7.6	1721	3	US-08-700-651-5	Sequence 5, Appl
19	175	7.6	1721	3	US-08-928-361B-6	Sequence 6, Appl
20	175	7.6	1721	4	US-08-588-995A-6	Sequence 6, Appl
21	173.5	7.6	448	4	US-09-248-796A-14116	Sequence 14116, A
22	169.5	7.4	426	4	US-09-248-796A-14114	Sequence 14114, A
23	164.5	7.2	176	4	US-09-248-796A-16696	Sequence 16696, A
24	157.5	6.9	171	4	US-09-248-796A-14120	Sequence 14120, A
25	155	6.7	894	3	US-08-362-525-22	Sequence 22, Appl
26	155	6.7	894	3	US-08-971-632-15	Sequence 15, Appl
27	154	6.7	522	4	US-08-971-632-15	Sequence 15, Appl
28	152	6.6	442	4	US-09-248-796A-14121	Sequence 14121, A
29	150.5	6.6	175	3	US-09-248-796A-26457	Sequence 26457, A
30	150.5	6.6	175	3	US-08-700-651-12	Sequence 12, Appl
31	150.5	6.6	175	4	US-08-928-361B-17	Sequence 17, Appl
32	150.5	6.6	288	4	US-09-588-995A-17	Sequence 17, Appl
33	150.5	6.6	288	4	US-09-216-333B-341	Sequence 341, App
34	149.5	6.6	288	4	US-09-216-333B-344	Sequence 344, App
35	148.5	6.5	529	4	US-09-248-796A-16703	Sequence 16703, A
36	148.5	6.5	216	3	US-08-928-361B-8	Sequence 8, Appl
37	148.5	6.5	216	3	US-09-588-995A-8	Sequence 8, Appl
38	146.5	6.4	249	3	US-08-325-267A-4	Sequence 4, Appl
39	146.5	6.4	249	3	US-08-700-651-15	Sequence 15, Appl
40	146.5	6.4	249	4	US-08-928-361B-20	Sequence 20, Appl
41	145	6.3	130	3	US-09-588-995A-20	Sequence 20, Appl
42	145	6.3	130	3	US-08-700-651-9	Sequence 9, Appl
43	145	6.3	130	3	US-08-928-361B-14	Sequence 14, Appl
44	144.5	6.3	3892	4	US-09-588-995A-14	Sequence 14, Appl
45	144	6.3	827	4	US-09-328-352-5503	Sequence 5503, Ap
					US-09-248-796A-17307	Sequence 17307, A

ALIGNMENTS

RESULT 1

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US-09-248-796A-16243
; Sequence 16243, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO
; TITLE OF INVENTION: FOR DIAGNOSTICS AND T
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16243
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16243

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Alignment Scores:

Alignment Score:	
Pred. No.:	1,32e-194
Score:	2170.00
Length:	1151
Matches:	411
Percent Similarity:	99.52%
Conservative:	2
Best Local Similarity:	99.04%
Mismatches:	2
Query Match:	4
Indels:	0
Gaps:	0
DB:	

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20 LysThrIleThrGlyValPheAspSerPheAsnSerLeuThrTrpSerAsnAlaAAsn 39

QY 61 TATGCTTTCAAGGGCCAGGATACCCAACTTGAATGCTGTTTGGGTGGTCTTAGAT 120
Db 40 TyrAlaPheLysGlyProGlyTyrProThrTrpAsnAlaValLeuGlyTrpSerLeuAsp 59
QY 121 GGTACCAGTCCCAATCCAGGGATACATTCACATTGAATAGCCATGTGTTTAAATAT 180
Db 60 GlyThrSerAlaAsnProGlyAspThrPheThrLeuAsnMetProCysValPheArgTyr 79
QY 181 ACTACTTCACAAACATCTGTTGATTTAACTGCCGATGGTGTAAATATGCTACTCTCAA 240
Db 80 ThrThrSerGlnThrSerValAspLeuThrAlaAspGlyValLysTyrAlaThrCysGln 99
QY 241 TTTTATTCTGGTGAAGAATTCACAACTTTTCTACATTTAACTGATGTTGAACGAGCT 300
Db 100 PheTyrSerGlyGluGluPheThrPheSerThrLeuThrCysThrValAsnAspAla 119
QY 301 TTGAATCATCCATTAAGCATTTGGTACAGTTACGTTTACCAATTGCAATTCATTTGGT 360
Db 120 LeuLysSerSerIleLysAlaPheGlyThrValThrLeuProIleAlaPheAsnValGly 139
QY 361 GGAACAGGTTTCATCACTGATTTGGAGATTTCTAAATGTTTACTGCTGTCACCAATACA 420
Db 140 GlyThrGlySerThrAspValGluAspSerLysCysPheThrAlaGlyThrAsnThr 159
QY 421 GTCACATTTAATGATGTTGATAAGATATCTCAATGATGTTGAGTTTGAAGAAGTCAACC 480
Db 160 ValThrPheAsnAspGlyAspLysAspIleSerIleAspValGluPheGluLysSerThr 179
QY 481 GTTGATCCAAAGTGATATTTGATGCTTCAGAGTTATGCCAAGTCTCAATAAGTCCACA 540
Db 180 ValAspProSerGlyTyrLeuTyrAlaSerArgValMetProSerLeuAsnLysValThr 199
QY 541 ACTCTTTTCTGGCACCACACATGTGAAATGGTTTACACATCTGTCAATGGGTTCTCC 600
Db 200 ThrLeuPheValAlaProGlnCysGluAsnGlyTyrThrSerGlyThrMetGlyPheSer 219
QY 601 AGTAGTAACGGTGACGTTGCTATTGATTTGCTCAAAATATTCATATTTGATATCAAAAGGA 660
Db 220 SerSerAsnGlyAspValAlaIleAspCysSerAsnIleHisIleGlyIleThrLysGly 239
QY 661 TTAATGATTTGGAATTAACGGTTTCATCTGAATCATTTAGTTAGTTACACTAAACTGTGACA 720
Db 240 LeuAsnAspTrpAsnTyrProValSerSerGluSerPheSerTyrThrLysThrCysThr 259
QY 721 TCTAATCGAATTCAGATTAAATATCAAAATGTACTGCTGTTATCTGCTCAATTTATTGAT 780
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QY 781 GCTTATATTTCTGTACAGATGTTTAAACCAATATATCTTTAGCATATACCAATGATTTACT 840
Db 280 AlaTyrIleSerAlaThrAspValAsnGlnTyrThrLeuAlaTyrThrAsnAspTyrThr 299
QY 841 TGCTGCGGAGTCTGTCGAAGTAAACCTTTCACTTTAGATGGAGTCAATCAAGAAT 900
Db 300 CysAlaGlySerArgLeuGlnSerLysPheThrLeuArgTrpThrGlyTyrLysAsn 319
QY 901 AGTCATCCGATCTAAGGATTTGTCATTTGCTACAACTAGACAGTTTACAGACAGT 960
Db 320 SerAspAlaGlySerAsnGlyIleValIleValAlaThrThrArgThrValThrAspSer 339
QY 961 ACCACTGCTGTCACTACTTTACCAATCCAAATCCAAAGTGTGATAAAACCAAAATCGAA 1020
Db 340 ThrThrAlaValThrThrLeuProPheAsnProSerValAspLysThrLysThrIleGlu 359
QY 1021 ATTTTGCACTTATCCAACTACCATTCACAACTTCATATGTTGGTGTGACTACTTCC 1080
Db 360 IleLeuGlnProIleProThrThrThrIleThrThrSerTyrValGlyValThrThrSer 379
QY 1081 TATCTGACTAAGACTGCACCAATTTGGTGAACACACTACTGTTATTTGATGTGCCATAT 1140
Db 380 TyrLeuThrLysThrAlaProIleGlyGluThrAlaThrValIleValAspValProTyr 399
QY 1141 CATACTACCACTGTTTACCGATGAATGGACAGGAACAATTCACTACCAACCACTCGT 1200

Db 400 HisThrThrThrThrValThrSerGluTrpThrGlyThrIleThrThrThrThrArg 419
QY 1201 ACCAATCCAACTGATTCAATTCACAGTGGGTGACAGTTTCCA 1245
Db 420 ThrAsnProThrAspTyrIleAspThrValValGlnValPro 434
RESULT 2
US-09-248-796A-16702
; Sequence 16702, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16702
; LENGTH: 780
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (493)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unk
US-09-248-796A-16702

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Pred. No.: 2,73e-169 Length: 780
Score: 1899.00 Matches: 357
Percent Similarity: 91.33% Conservative: 22
Best Local Similarity: 86.02% Mismatches: 36
Query Match: 82.67% Indels: 0
DB: 4 Gaps: 0

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QY 61 TATGCTTTCAAGGGCCAGGATACCCAACTTGAATGCTGTTTGGGTGGTCTTAGAT 120
Db 40 TyrAlaPheLysGlyProGlyTyrProThrTrpAsnAlaValLeuGlyTrpSerLeuAsp 59
QY 121 GGTACCAGTCCCAATCCAGGGATACATTCACATTCGAATATGTCATGTGTGTTTAAATAT 180
Db 60 GlyThrSerAlaAsnProGlyAspThrPheIleLeuAsnMetProCysValPheLysPhe 79
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Db 80 ThrAlaSerGlnLysSerValAspLeuThrAlaAspGlyValLysTyrAlaThrCysGln 99
QY 241 TTTTATTCTGGTGAAGAATTCACAACTTTTCTACATTTAACTGATGTTGAACGAGCT 300
Db 100 PheTyrSerGlyGluGluPheThrPheSerSerLeuLysCysThrValAsnAsnAsn 119
QY 301 TTGAATCATCCATTAAGCATTTGGTACAGTTTACAGTTTACTTTTACCAATTCATTTGTTGGT 360
Db 120 LeuArgSerSerIleLysAlaLeuGlyThrValThrLeuProIleAlaPheAsnValGly 139
QY 361 GGAACAGGTTTCATCACTGATTTGGAGATTTCTAAATGTTTACTGCTGTCACCAATACA 420
Db 140 GlyThrGlySerSerValAspLeuGluAspSerLysCysPheThrAlaGlyThrAsnThr 159
QY 421 GTCACATTTAATGATGTTGATAAGATATCTCAATTTGATGTTGAGTTTGAAGAAGTCAACC 480

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Db 160 ValThrPheAsnAspGlySerLysLysLeuSerIleAlaValAsnPheGluLysSerThr 179
QY 481 GTTGATCCAGTGCATATTTGTATGCTTCCAGAGTTATGCCAAGTCTCAATAAGGTCA 540
Db 180 ValAspGlnSerGlyThrLeuThrThrSerArgPheMetProSerLeuAsnLysIleAla 199
QY 541 ACTCTTTTGTGGCACCACAAATGTTGAAATGGTTACACATCTGGTACAAATGGGTTCTCC 600
Db 200 ThrLeuThrValAlaProGlnCysGluAsnGlyThrSerGlyThrMetGlyPheSer 219
QY 601 AGTAGTAACGGTGAGCTGTATGATGCTCAATATTCATATTCATATTCATATTCATATTC 660
Db 220 ThrSerThrGlyAspValAlaIleAspCysSerAsnValHisIleGlyIleSerLysGly 239
QY 661 TTAATGATGGATATTCGGTTTCATCTCAATCATTCATCTACACTTAAACATTTGTACA 720
Db 240 ValAsnAspTrpAsnHisProValThrSerGluSerPheSerThrLysSerCysSer 259
QY 721 TCTAATGGAATTCAGATTAAATATCAAAATGTACTGCTGTTATCTGCTCAATTTATGAT 780
Db 260 SerPheGlyIleSerIleThrThrGlnAsnValProAlaGlyThrArgProPheIleAsp 279
QY 781 GCTTATATTTCTGCTACAGATGTTAAACCAATATCTTACATATACCAATGATATATCT 840
Db 280 AlaTyrlleSerProSerAspAsnAsnGlnTyrlleGlnLeuSerTyrlleAsnAspTyrlle 299
QY 841 TGTGCTGGCAGTCTCTCAAGATTAACCTTTCATCTTAAAGTGAAGTGAAGTGAAGTGA 900
Db 300 CysValAspAspTyrlleGlnHisAlaProPheThrLeuArgTrpThrGlyThrLysAsn 319
QY 901 AGTAGTCCGGATCTPAACGGTATTGTCAATGTCTGCTACCACTAGAACAGTTTACAGACGT 960
Db 320 SerAspAlaGlySerAsnGlyIleValIleValAlaThrThrArgThrValThrAspSer 339
QY 961 ACCACTGCTGCTACTTTTACCAATCAATCAAGTGTGTATAAAACCAACCAATCGAA 1020
Db 340 ThrThrAlaValSerThrLeuProPheAsnProSerValAspLysThrLysThrIleGlu 359
QY 1021 ATTTTGAACCTATTCACCACTACCACTACCACTTCAATGTTGTTGTTGTTGTTGTTG 1080
Db 360 IleLeuGlnProIleProThrThrThrIleThrThrSerTyrlleValGlyValThrSer 379
QY 1081 TATCTGACTTAAGACTGCACCAATGCTGCAACAGCTACTGTTATTTGTTGTTGTTGTTG 1140
Db 380 TyrLeuThrLysThrAlaProIleGlyIleThrAlaThrValIleValAspValProTyrlle 399
QY 1141 CATACTACCACTGTTTACCAGTGAATGGACAGGACCAATCACTTACCACTTACCACTTCC 1200
Db 400 HisThrThrThrThrValThrSerGluTrpThrGlyThrThrThrThrThrThrArg 419
QY 1201 ACCAATCCACTGATTCATTCAGACAGTGGTGGTACAGTTCCA 1245
Db 420 ThrAsnProAsnAspSerIleAspThrValValGlnValPro 434
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RESULT 3

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US-09-248-796A-14125
; Sequence 14125, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14125
; LENGTH: 511
; TYPE: PRN
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; ORGANISM: Candida albicans
US-09-248-796A-14125
Alignment Scores:
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Score: 1599.00 Matches: 294
Percent Similarity: 81.45% Conservative: 44
Best Local Similarity: 70.84% Mismatches: 77
Query Match: 69.61% Indels: 0
DB: 4 Gaps: 0
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US-09-715-876-7_COPY_52_1296 (1-1245) x US-09-248-796A-14125 (1-511)

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QY 61 TATGCTTTCAAGGGCCAGGATACCCAACTTGGATGCTGTTTGGGTTGGTCTTATAT 120
Db 46 TyrSerTyrlleArgGlyProAlaAsnProThrTrpThrAlaValIleGlyTrpSerLeuAsp 65
QY 121 GGTACCACTGCCAATCCAGGGGATACATTACATTGAATATGCTGTTGTTTAAATAT 180
Db 66 GlyAlaThrAlaSerAlaGlyAspThrPheThrLeuAspMetProCysValPheLysPhe 85
QY 181 ACTACTTTCACAAACATCTGTTGATTTAACTGCCGATGCTGTTAAATATGCTTACTTGTCAA 240
Db 86 IleThrAspGlnThrSerIleAspLeuValAlaAspGlyArgThrThrAlaThrCysAsn 105
QY 241 TTTTATTTCTGGTGAAGAATTCAACATTTTCTTACATTAATCATGCTACTGTGACGACGCT 300
Db 106 LeuAsnSerAlaGluGluPheThrThrPheSerSerValSerCysThrValThrThr 125
QY 301 TTGAATATCATCCATTAGGCAATTTGGTACAGTTACTTTTACCAATGCTGCTCAATGTTGGT 360
Db 126 MetThrAlaAspThrLysAlaIleGlyThrValThrLeuProPheSerPheSerValGly 145
QY 361 GGAACAGTTCATCAACTGATTTTGAAGATTTTAAATGTTTACTGCTGGTACCAATACA 420
Db 146 GlySerGlySerAspValAspLeuAlaAsnSerGlnCysPheThrAlaGlyIleAsnThr 165
QY 421 GTCACATTTAATGATGTGATAAAGATATCTCAATGATGATGTTGATTTGAAAGTCAACC 480
Db 166 ValThrPheAsnAspGlyAspThrSerIleSerAlaThrValAlaAspPheGluLysSerThr 185
QY 481 GTTCATCCAACTGCATATTTGTATGCTTCCAGACTTATGCCAAGTCTCAATTAAGTCCACA 540
Db 186 ValAlaSerSerAspArgIleLeuLeuSerArgIleLeuProSerLeuSerGlnAlaVal 205
QY 541 ACTCTTTTGTGGCACCACCAATGTTGAAATGGTTTACACATCTGCTGATCAATGGGTTCTCC 600
Db 206 SerLeuPheLeuProGlnGluCysAlaAsnGlyThrThrSerGlyThrMetGlyPheSer 225
QY 601 AGTAGTAACGGTGAAGTGTATGATGCTCAATATTCATATTCATATTCATATTCATATTC 660
Db 226 ThrAlaGlyThrGlyAlaThrIleAspCysSerThrValHisValGlyIleSerAsnGly 245
QY 661 TTAATGATGGATTTATCCGTTTTCATCTGAATCATTTAGTACTTACACTTAAATGTTGATCA 720
Db 246 LeuAsnAspTrpAsnTyrlleSerLeuGluSerPheSerThrLysThrCysThr 265
QY 721 TCTAATGGAATTCAGATTAAATATCAAAATGTACTGCTGTTATCTGCTCAATTTATGAT 780
Db 266 SerThrSerValLeuValThrThrGlnAsnValProAlaGlyThrArgProPheValAsp 285
QY 781 GCTTATATTTCTGCTACAGATGTTTAAACCAATATATCTTACATATACCAATGATATATCT 840
Db 286 AlaTyrlleSerAlaThrArgValSerSerTyrlleAlaMetArgTyrlleThrAsnIleTyrlle 305
QY 841 TGTGCTGGCAGTCTCTGCAAGATTAACCTTTCATCTTAAAGTGAAGTGAAGTGAAGTGA 900
Db 306 CysValGlyAlaAlaSerValAspAspSerPheThrHisThrTrpLeuGlyTyrlleSerAsn 325
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QY      826  ACCAATGATTATCTTGTGCTGGCAGTCGTCGCAAGTAACCTTTCACTTTAAGATGG 885
Db      107  ThrAsnAspTyrAlaCyValGlySerSerLeuGlnSerLysProPheAsnLeuArgLeu 126
QY      886  ACTGGATACAAGATAGTATGCGGATCTAAGTATGTCATTTGTTGTCACAACATAGA 945
Db      127  ArgGlyTyrAsnAsnSerGluAlaAsnSerAsnGlyPheValIleValAlaThrThrArg 146
QY      946  ACAGTTACAGACAGTACCACTGCTGCTACCTACTTTACCACTTCAATCAAGTGTGATAA 1005
Db      147  ThrValThrAspSerThrThrAlaValThrLeuProPheAsnProSerIleAspLys 166
QY      1006  ACCAAAAACAATCGAAATTTTGCAACCTATTCACCACTACCACTCAAACTTCATATGTT 1065
Db      167  ThrLysThrIleGluIleLeuGlnProIleProThrThrThrThrThrThrThrThrVal 186
QY      1066  GGTGTGACTACTTCCTACTGCTAAGCACTGACAGTGCACCAATGCGTGAACAGACTACTGTTAT 1125
Db      187  GlyValSerThrSerTyrLeuThrLysThrAlaProIleGlyGluThrAlaThrValIle 206
QY      1126  GTTGATGCGCATATCATCTACCACTGCAAGCACTGTTACCACTGAATGGACAGCAACATCACT 1185
Db      207  ValAspValProTyrHisThrThrThrThrValThrSerGluThrThrGlyThrIleThr 226
QY      1186  ACCACCAACAACCTGCTACCAATCCAACTGATTCATTCATTCACAGTGGTGGTACAACTTCCA 1245
Db      227  ThrThrThrThrArgThrAsnProThrAspSerIleAspThrValValGlnValPro 246

RESULT 7
US-09-248-796A-16244
; Sequence 16244, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16244
; LENGTH: 812
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16244

Alignment Scores:
Pred. No.: 1,45e-83 Length: 812
Score: 984.50 Matches: 194
Percent Similarity: 63.46% Conservative: 70
Best Local Similarity: 46.63% Mismatches: 151
Query Match: 42.86% Indels: 1
DB: Gaps: 4

US-09-715-876-7_COPY_52_1296 (1-1245) x US-09-248-796A-16244 (1-812)
QY      1  AAGACAATCACTGCTGTTTGTAGATGTTTAAATTCATTAACCTGGTCCAAATGCTGTAAT 60
Db      29  LysGluValThrGlyValPheAsnGlnPheAsnSerLeuIleTyrSerTyrThrTyrArg 48
QY      61  TATGCTTTCAAGCGCCAGGATACCCAACTTGGAATGCTGTTGGGTGGTCTTATAGAT 120
Db      49  AlaArgTyrGluGluIleSerThrLeuThrAlaLysAlaGlnLeuGluTyrAlaLeuAsp 68
QY      121  GGTACCAAGTGCATTCAGGGGATACATTCATTTGAATATGCCATGCTGGTGTAAATAT 180
Db      69  GlyThrIleAlaSerProGlyAspThrPheThrLeuValMetProCysValTyrLysPhe 88
QY      181  ACTACTTCACAAACATCTGTTGATTTAACTGCCGATGGTGTAAATATATGCTACTTGTCAA 240
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Db      89  MetThrTyrGluThrSerValGlnLeuThrAlaAsnSerIleAlaTyrAlaThrCysAsp 108
QY      241  TTTTATCTCTGGTGAAGAATTCACAACTTTTCTACATTAACATGCTACTGCTGAACGACGCT 300
Db      109  PheAspAlaGlyGluAspThrLysSerPheSerSerLeuLysCysThrValThrAspGlu 128
QY      301  TTGAATCATCATCAATTAAGGCATTTTGTACAGTTTACTTTACCAATTTGCATTTCAATGTTGT 360
Db      129  LeuThrGluAspThrSerValPheGlySerValIleLeuProIleAlaPheAsnValGly 148
QY      361  GGAACAGGTTCACTCAACTGATTTTGAAGATTCCTAAATGTTTACTCTGCTGGTACCAATACA 420
Db      149  GlySerGlySerLysSerThrIleThrAspSerLysCysPheSerSerGlyTyrAsnThr 168
QY      421  GTCACATTTAATCATGCTGATAAAGATATCTCAATTTGATGTTGAGTTTCAAAAGTCAACC 480
Db      169  ValThrPhePheAspGlyAsnAsnGlnLeuSerThrThrAlaAsnPheLeuProArgArg 188
QY      481  GTTGATCCCAAGTGCATATTTTGTATGCTTCAGAGTTATGCCAAGTCTCAATTAAGGTCACA 540
Db      189  GluLeuAlaPheGlyLeuValSerGlnArgLeuSerMetSerLeuAspThrMetThr 208
QY      541  ACTCTTTTGTGGCACCACAAATGCGAAATGGTTACACATCTGCTGCTACCAATGGGTTCTCC 600
Db      209  AsnPheValMetSerThrProCysPheMetGlyTyrGlnLeuGlyLysLeuGlyPheThr 228
QY      601  AGTAGTAACGGTGCACCTGCTATGCTCAATATTCATATTCATATTCATATTCACAAAGGA 660
Db      229  SerAsnAspAspAspPheGluIleAspCysSerSerIleHisValGlyIleThrAsnGlu 248
QY      661  TTAATATGATGGAATTTATCCGGTTTCATCTGAATCATTTAGTTTACATAAACTTGTACA 720
Db      249  IleAsnAspTyrSerMetProValSerSerValProPheAspHisThrIleArgCysThr 268
QY      721  TCTAATGGAATTCAGATTAATATCAAAATGCTACCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db      269  SerArgAlaLeuTyrIleGluPheLysThrIleProAlaGlyTyrArgProPheValAsp 288
QY      781  GCTATATTTCTGCTACAGATGTTAACCAATATCTATTAGCATATATACCAATGATTATACT 840
Db      289  AlaIleValGlnIleProThrThrGluProPhePheValLysTyrThrAsnGluPheAla 308
QY      841  TGTGCTGGCAGTCTGCTGCAAAAGTAAACCTTTACCTTTTAAAGATGGAT---GGATACAAG 897
Db      309  CysValAsnGlyIleTyrThrSerIleProPheThrSerPhePheSerGlnProIleLeu 328
QY      898  AATAGTGTATGCCGATCTAACGGTATTGTCATTTGCTTACACTAGACAGTTCACAGAC 957
Db      329  TyrAspGluAlaLeuAlaIleGlyAlaAspLeuValArgThrThrSerThrValIleGly 348
QY      958  AGTACCACCTGCTGCTCACTACTTTTACCATTCAATCCAAAGTGTGATATAAAACCAAAATC 1017
Db      349  SerIleThrArgThrThrThrLeuProPheIleSerArgLeuGlnLysThrLysThrIle 368
QY      1018  GAAATTTGCAACCTATTCACCACTACATCACAACCTTCATATCATATTTGCTGCTGCTACT 1077
Db      369  LeuValLeuGluProIleProThrThrThrValThrThrSerHisGlyPheAspThr 388
QY      1078  TCTATCTGACTTAAGACTGCACCAATTTGTTGAACAGCTACTGTTATTTGTTGATGTGCCA 1137
Db      389  TrpTyrTyrThrLysLysAlaThrIleGlyAspThrAlaThrValPheIleAspValPro 408
QY      1138  TATCATACTACCACTGTTTACCACTGAATGACAGGAAACCAATCACTACCACTACCAACT 1197
Db      409  GlnHisThrAlaThrThrLeuThrThrTyrTyrTyrGlnGluSerSerThrAlaThrThr 428
QY      1198  CGTACCACCACTCAATCAATTTGACAGTGGTGGTGCACAGTTCCA 1245
Db      429  TyrPheAspAspIleAspLeuValAspThrValIleValLysIlePro 444

RESULT 8
US-09-248-796A-16698
```

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; Sequence 16698, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16698
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16698

Alignment Scores:
Pred. No.: 7,7e-68 Length: 229
Score: 814.00 Matches: 154
Percent Similarity: 86.93% Conservative: 19
Best Local Similarity: 77.39% Mismatches: 26
Query Match: 35.44% Indels: 1
DB: 4 Gaps: 0

US-09-715-876-7_COPY_52_1296 (1-1245) x US-09-248-796A-16698 (1-229)
QY 1 AAGACAATCACTGGTGTGTTTGGATAGTTTAAATTCATTAACTGGTCCAAATGCTGCTAAT 60
DB 26 LysValIleThrGlyValPheAsnSerPheAspSerLeuThrTrpThrArgAlaGlyAsn 45
QY 61 TATGCTTTCAAGGCCAGGATACCCAACTTGGAAATGCTGTTTGGGTGGTCTTAGAT 120
DB 46 TyrAlaTyrLysGlyProAsnArgProThrTrpAsnAlaValLeuGlyTrpSerLeuAsp 65
QY 121 GGTACAGTGCACATCCAGGGGATACATTCACATTAATGATGCGATGCTGTTAAATAT 180
DB 66 GlyThrSerAlaAsnProGlyAspThrPheThrLeuAsnMetProCysValPheLysPhe 85
QY 181 ACTACTTCACAACTCTGTCATTTTAACTGCGGATGTTTAAATATGCTACTTGTCAA 240
DB 86 IleThrAspGlnThrSerValAspLeuThrAlaGluGlyValLysThrAlaThrCysGln 105
QY 241 TTTTATCTCGTGAAGAATTCAAACTTTTCTACATTAACATGATGCTGTAACGACGCT 300
DB 106 PheTyrSerGlyGluGluPheThrPheSerSerLeuLysCysThrValSerAsnThr 125
QY 301 TTGAATATCATCAATTAAGGCATTTGGTACAGTTACTTTACCAATTTGCAATTCATGTTGGT 360
DB 126 LeuThrSerSerIleLysAlaLeuGlyThrValThrLeuProIleSerPheAsnValGly 145
QY 361 GGAACAGGTTTCATCACTGATTTGGAGATTTCTAATGTTTACTGCTGGTACCATAACA 420
DB 146 GlyThrGlySerSerValAspLeuGluAsnSerGlnCysPheLysAlaGlyThrAsnThr 165
QY 421 GTCACATTTAATGATGTCATTAAGATATCTCAATTTGATGTTGAGTTTGAAAGTCAACC 480
DB 166 ValThrPheAsnAspGlyAspLysLysIleSerIleAspValAspPheGluLysThrAsn 185
QY 481 GTTGATCCCAAGTCATATTTGATGCTTCCAGATTTATGCCAGTCTCAATTAAGTCAAC 540
DB 186 GluAspAlaSerGlyTyrPheIleAlaSerArgLeuIleProSerIleAsnLysAlaSer 205
QY 541 ACTCTTTTGTGGC-ACCACATGTCGAAATGTTTACATCTGGTACCAATGGGTT 596
DB 206 IleThrTyrValAlaThrThrMetCysLysTrpLeuHisIleTrpCysAsnGlyVal 224

RESULT 9
US-09-248-796A-14122
; Sequence 14122, Application US/09248796A
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; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14122
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-14122

Alignment Scores:
Pred. No.: 3,23e-47 Length: 232
Score: 594.00 Matches: 111
Percent Similarity: 79.50% Conservative: 17
Best Local Similarity: 68.94% Mismatches: 33
Query Match: 25.86% Indels: 0
DB: 4 Gaps: 0

US-09-715-876-7_COPY_52_1296 (1-1245) x US-09-248-796A-14122 (1-232)
QY 1 AAGACAATCACTGGTGTGTTTGGATAGTTTAAATTCATTAACTGGTCCAAATGCTGCTAAT 60
DB 71 LysThrIleThrGlyValPheAsnSerPheAspSerLeuThrTrpThrArgSerValGlu 90
QY 61 TATGCTTTCAAGGCCAGGATACCCAACTTGGAAATGCTGTTTGGGTGGTCTTAGAT 120
DB 91 TyrValTyrLysGlyProGluThrProThrTrpAsnAlaValLeuGlyTrpSerLeuAsn 110
QY 121 GGTACAGTGCACATCCAGGGGATACATTCACATTAATGATGCTGTTTAAATAT 180
DB 111 SerThrThrAlaAspProGlyAspThrPheAsnLeuIleLeuProCysValPheLysPhe 130
QY 181 ACTACTTCACAACTCTGTTGATTTAACTGCGGATGTTTAAATATGCTACTTGTCAA 240
DB 131 IleThrThrGlnThrSerValAspLeuThrAlaAspGlyValSerTyrAlaThrCysAsp 150
QY 241 TTTTATCTCGTGAAGAATTCAAACTTTTCTACATTAACATGATGCTGTAACGACGCT 300
DB 151 PheAsnAlaGlyGluGluPheThrThrPheSerSerLeuSerCysThrValAsnSerVal 170
QY 301 TTGAATATCATCAATTAAGGCATTTGGTACAGTTACTTTTACCAATTTGCAATTCATGTTGGT 360
DB 171 SerValSerTyrAlaArgValSerGlyThrValLysLeuProIleThrPheAsnValGly 190
QY 361 GGAACAGGTTTCATCACTGATTTGGAGATTTCTAATGTTTACTGCTGGTACCATAACA 420
DB 191 GlyThrGlySerSerValAspLeuAlaAspSerLysCysPheThrAlaGlyLysAsnThr 210
QY 421 GTCACATTTAATGATGTCATTAAGATATCTCAATTTGATGTTGAGTTTGAAAGTCAACC 480
DB 211 ValThrPheMetAspGlyAspThrLysIleSerThrThrValAspPheAspAlaSerPro 230
QY 481 GTT 483
DB 231 Val 231

RESULT 10
US-09-248-796A-14119
; Sequence 14119, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBIC
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
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/ FILE REFERENCE: 107196.132
/ CURRENT APPLICATION NUMBER: US/09/248,796A
/ CURRENT FILING DATE: 1999-02-12
/ PRIOR APPLICATION NUMBER: US 60/074,725
/ PRIOR FILING DATE: 1998-02-13
/ PRIOR APPLICATION NUMBER: US 60/096,409
/ PRIOR FILING DATE: 1998-08-13
/ NUMBER OF SEQ ID NOS: 28208
/ SEQ ID NO 14119
/ LENGTH: 154
/ TYPE: PRT
/ ORGANISM: Candida albicans
US-09-248-796A-14119

Alignment Scores:
Pred. No.: 2,87e-46 Length: 154
Score: 583.00 Matches: 111
Percent Similarity: 83.44% Conservative: 15
Best Local Similarity: 73.51% Mismatches: 25
Query Match: 25.38% Indels: 0
DB: 4 Gaps: 0

US-09-715-876-7_COPY_52_1296 (1-1245) x US-09-248-796A-14119 (1-154)
Qy 679 CCGGTTTCATCATGAATCAATTTAGTACACATAAACTTGATCATCAATGAATTCAGATT 738
Db 4 ProglySerSerGluSerPheSerTyThrLysThrCysThrSerThrSerIleThrVal 23
Qy 739 AATATCAAAATGATCTGCTGCTGTTATCGCCATTTATTCATGCTTATATTTCTGTACA 798
Db 24 GluPheGlnAsnValProAlaGlyTyArgProPheValAspAlaTyIleSerAlaGlu 43
Qy 799 GATGTTAACCAATATCTTTAGCATATACCAATGATTATCTTGCTGCGAGTCGTCG 858
Db 44 AsnIleAspLysTyThrLeuThrTyAlaAsnGluTyThrCysGluAsnGlyAsnThr 63
Qy 859 CAAAGTAAACCTTTCACTTTAAGATGGACTGGATACAAAGATAGTATGCGGATCTAAC 918
Db 64 ValValAspProPheThrLeuThrTyrTyrGlyTyIleAsnSerGluAlaAspSerAsp 83
Qy 919 GGTATTCATTTGTTGCTACACAGTACAGTACAGTACAGTACAGTACAGTACAGTACT 978
Db 84 GlyAspValIleValThrArgThrArgThrValThrAspSerThrThrAlaValThrThr 103
Qy 979 TTACATTCATCAACGTTGTGATAAAACCAAAACCAATCGAAATTTTGCAACCTATCCA 1038
Db 104 LeuProPheAsnProSerValAspLysThrGluThrIleGluIleLeuGlnProIlePro 123
Qy 1039 ACCATCACTACCAACTTCATATGTTGGTGTGACTACTTCCTATCTGACTAAGACGCA 1098
Db 124 ThrThrIleThrThrSerTyIleGlyIleSerThrSerTyGluThrLeuThrGly 143
Qy 1099 CCAATTCGTGAACAGTACTGTTATGTTGAT 1131
Db 144 ThrIleGlyGlyThrAlaThrValIleValAsp 154

RESULT 11
US-08-362-525-2
/ Sequence 2, Application US/08362525
/ Patent No. 6027910
/ GENERAL INFORMATION:
/ APPLICANT: KLIS, FRANCISCUS M.
/ APPLICANT: SCHREUDER, MAARTEN P.
/ APPLICANT: TOSCHKA, HOLSER Y.
/ APPLICANT: VERRIPS, CORNELIS T.
/ TITLE OF INVENTION: PROCESS FOR IMMOBILIZING ENZYMES TO THE
/ CELL WALL OF A MICROBIAL CELL BY PRODUCING A FUSION
/ PROTEIN
/ NUMBER OF SEQUENCES: 26
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: CUSHMAN DARB & CUSHMAN, L.L.P.
/ STREET: 1100 New York Avenue, N.W.
/ CITY: Washington
```

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/ STATE: D. C.
/ COUNTRY: U.S.A.
/ ZIP: 20005-3918
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/362,525
/ FILING DATE: 04-JAN-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 92202080.5
/ FILING DATE: 08-JUL-1992
/ PRIOR APPLICATION NUMBER: EP 92203899.7
/ FILING DATE: 14-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/EP93/01763
/ FILING DATE: 07-JUL-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: KOKULIS, PAUL N.
/ REGISTRATION NUMBER: 16,773
/ REFERENCE/DOCKET NUMBER: 213289/T7020(V)
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 861-3000
/ TELEFAX: (202) 822-0944
/ TELEX: 6714627 CUSH
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 650 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-362-525-2

Alignment Scores:
Pred. No.: 3e-20 Length: 650
Score: 308.50 Matches: 116
Percent Similarity: 43.33% Conservative: 79
Best Local Similarity: 25.78% Mismatches: 190
Query Match: 13.43% Indels: 65
DB: 3 Gaps: 20

US-09-715-876-7_COPY_52_1296 (1-1245) x US-08-362-525-2 (1-650)
Qy 25 AGTTTAAATTCATTAATCTGTTGCTCAAT-----GCTGCTAATATGCT 66
Db 21 AsnIleAsnAspIleThrPheSerAsnLeuGluIleThrProLeuThrAlaAsn----- 38
Qy 67 TTCAAGGGCCAGGATACCAACTTGAATGCTGTTTGGTGGTCTTAA---GATGGT 123
Db 39 ---LysGlnProAsp---GlnGlyThrThrAlaThrPheAspPheSerIleAlaAspAla 56
Qy 124 ACCAGTCCCAATCCAGGGGATACATTCACATTAATGATGCTGTTTAA----- 177
Db 57 SerSerIleArgGluGlyAspGluPheThrLeuSerMetProHisValTyArgIleLys 76
Qy 178 ---TATACACTTCACAAACATCTGTTGATTTAACTGCCGATGCTGTTAAATGCTACT 234
Db 77 LeuLeuAsnSerSerGlnThrAlaThrIleSerLeuAlaAspGlyThrGluAlaPheLys 96
Qy 235 TGTCAATTTTATCTGCTGAA-----GAATTCACAACTTTTCTACATTA 279
Db 97 Cys---TyrValSerGlnGlnAlaAlaTyThrLeuTyThrGluAsnThrThrPhe----- 112
Qy 280 ACATGATCTGTGAACGACGCTTTGAAATCATCATTAAGGCATTTGGTACAGTACTTTA 339
Db 113 ThrCysThrAlaGlnAsnAspLeuSerSerTyAsnThrIleAspGlySerIleThrPhe 132
Qy 340 CCAATTCATTCATCTGTTGGTGAACAGGTTTCATCACTGATTTGGAAGATTCCTAAATGT 399
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Db 133 SerLeuAsnPheSerAspGlySerSerTyrGluTyrGluLeuGluAsnAlaLysPhe 152
Qy 400 TTTACTGCTGTTACCAATACAGTCACATTTAATGATGATGATGATGATGATGATGAT 459
Db 153 PheLysSerGlyProMetLeuValLysLeuGluAsnGlnMetSerAspVal----- 169
Qy 460 GTTTCAGTTTGAAGAAGTCAACGGTTGATCCAAAGTGCATAT-----TTGATGCTTCC 510
Db 170 ValAsnPhe-----AspProAlaAlaPheThrGluAsnValPheHisSer 184
Qy 511 AGAGTTATGCCAAGTCTCAATAAGTCAACTCTTTTGGGACCAACCAATGTGAAT 570
Db 185 GlyArgSerThrGlyTyrGlySerPheGluSerTyrHisLeuGlyMetTyrCysProAsn 204
Qy 571 GGTTCACATCTGTT-----ACAATGGGTTCTCCAGTGTAGTAAACGGTGGCTT 621
Db 205 GlyTyrPheLeuGlyGlyThrGluLysIleAspTyrAspSerSerAsnAsnValAsp 224
Qy 622 ATTGATTGCTCAATATTATATTTGGTATCAAAAGGATTAATGATTTGGAATATCCG 681
Db 225 LeuAspCysSerSerValGlnValTyrSerSerAsnAspPheAsnAspTyrTyrPhePro 244
Qy 682 GTTTCATCTGAATCATTTAGTTACACTAAACTTGTACATCTAATGGAATTCAGATTAA 741
Db 245 GlnSerTyrAsnAspThrAsnAlaAspValThrCysPheGlySerAsnLeuTyrPheThr 264
Qy 742 TAT---CAAAATGATCTGCTGTTATCGTTCATTTATGATGCTTATATTTCT---GCT 795
Db 265 LeuAspGluLysLeuTyrAspGlyGluMetLeuTyrValAsnAlaLeuGlnSerLeuPro 284
Qy 796 ACAGATGTTTAAACCAATATCTTTAGCATATACCAATGATTTATCTTTGTT----- 843
Db 285 AlaAsnValAsnThrIleAspHisAlaLeuGluPheGlnTyrThrCysLeuAspThrIle 304
Qy 844 GCTGTCAGTCTGCTGCAAGTAACCTTTTCACTTTTAAAG-----TGGACTGGA 891
Db 305 AlaAsnThrThrTyrAlaThrGlnPheSerThrThrArgGluPheIleValTyrGlnGly 324
Qy 892 TACAAGATAGTAGTCCGGATCTAACCGTATTGTCATTTGCTTACAACTAGACAGTT 951
Db 325 ArgAsnLeuGlyThrAlaSerAlaLysSerSerPheIleSerThrThrThrAspLeu 344
Qy 952 ACAGAC-----AGTACCAGTCTGCTGCTACCTACTTTTACCATTTCAATCCCA 993
Db 345 ThrSerIleAsnThrSerAlaTyrSerThrGlySerIleSerThrVal----- 360
Qy 994 AGTGTGTATAAACCAACCAATCGAAATTTGCAACCTATTCCAACTACCATCCACA 1053
Db 361 GluThrGlyAsnArgThrThrSerGluValIleSerHisValValThrThrSerThrLys 380
Qy 1054 ACTTCATATGTTGGTGACTACTTCTCTATCTGACTAGACTGACCAATGGTGAACA 1113
Db 381 LeuSerProThrAlaThrThrSerLeuThrIleAlaGlnThrSerIleTyrSerThrAsp 400
Qy 1114 GCTACTGTTATTGTTGATGTCATATCATATCATACACA----- 1152
Db 401 SerAsnIleThrValGlyThrAspIleHisThrThrSerGluValIleSerAspValGlu 420
Qy 1153 ACTGTTACAGTGAATGACAGGAACAATCACTACCACTACCACTACCACTACCACT 1209
Db 421 ThrIleSerArgGluThrAlaSerThrValValAlaAlaProThrSerThrThrGlyTyr 440
Qy 1210 ACTGATTCATTTGACACAGTGGTGTACAA 1239
Db 441 ThrGlyAlaMetAsnThrTyrIleProGln 450

RESULT 12
US-09-248-796A-23586
; Sequence 23586, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 23586
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-23586
Alignment Scores: 3.64e-14 Length: 97
Pred. No.: 239.50 Matches: 54
Score: 67.39% Conservative: 8
Best Local Similarity: 58.70% Mismatches: 27
Query Match: 10.68% Indels: 3
DB: 4 Gaps: 1
US-09-715-876-7_COPY_52_1296 (1-1245) x US-09-248-796A-23586 (1-97)
Qy 494 GCACCTTGGATCA-----ACGTTTGACTTTTCAAACTCAACATCAATTTGAGATATCT 444
Db 6 AlaAlaGlySerGlyHisAspThrGlyAspAspSerLysSerThrValValGluIlePhe 25
Qy 443 TTATCACCATCATTAATGATGACTGTTATGGTACCAGCAGTAAACATTTAGATCTTCC 384
Db 26 ValSerProSerMetLysValThrValPhePheProAlaValLysHisLeuGluSerAla 45
Qy 383 AAATCAGTTGATGACCTGTTCCACCAACATTTGAATGCAATTTGTAAGTAAGTACCA 324
Db 46 LysSerThrGluGluProValProProThrLeuAsnValMetGlyAsnLeuThrValPro 65
Qy 323 AATGCCCTTAATGATGATTTCAAGCGCTGTTCCAGTACATGTTAATGTAGAAAAAGTT 264
Db 66 GluThrLeuAlaTyrAspThrGluThrLeuPheThrValHisAspLysGluGluAsnVal 85
Qy 263 GTGAATTTTCCACCAAGATAAATTTGACAAGTAGCA 228
Db 86 ValAsnSerSerProAlaLeuLysSerGlnValAla 97
RESULT 13
US-09-248-796A-14118
; Sequence 14118, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBIC
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14118
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-14118
Alignment Scores: 1.98e-09 Length: 501
Pred. No.: 192.50 Matches: 108
Score: 36.48% Conservative: 58
Best Local Similarity: 23.74% Mismatches: 170
Query Match: 8.38% Indels: 119


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Db 71 ArgGluProProAsnProThrValThrThrGluTyrTrpSerGlnSerTyrAlaThr 90
Qy 322 TTGGTACAGTACTTTACCAATTCGATTCAATGTTGGTGAACAGGTTCA----- 372
Db 91 ThrThrThrValThrAlaPro-----ProGlyGlyThrAspSerValIlelle 106
Qy 373 -----TCAACTGATTGGAAGATTCTAAATGTTTACTGCT 408
Db 107 ArgGluProProAsnProThrValThrThrGluTyrTrpSerGlnSerPhe---Ala 125
Qy 409 GGTACCAATCAGTCACATTAATGATGGTGAATAAGATATCTCAATGATGTTAGTTT 468
Db 126 ThrThrThrValThrAlaProProGlyGlyThrAspSerValIlelleArgGluPro 145
Qy 469 GAAAGTCAACCGTTGATCCAGTGCATATTGTTGATGCTTCCAGAGTTATGCCAAGTCTC 528
Db 146 ProAsnProThrValThrThrGluTyrTrpSerGlnSerTyrAla----- 161
Qy 529 AATAAGGTCACAACTCTTTTGTGGCCACCAATGTGAAATGTTACACATCTGTGTACA 588
Db 162 -----ThrThrThrValThrAlaProPro-----GlyGlyThrAspSerVal 176
Qy 589 ATGGGGTTCCTCAGTAGTAACGGTGCAGTGTGATGATGCTCAAAATATTCATATGGT 648
Db 177 IleIleArgGluProProAsnProThrValThr----- 188
Qy 649 ATCACAAGGATTAATGATGTAATATCCGGTTTCATCTGAATCATTTAGTTACACT 708
Db 189 -----ThrGluTyrTrp-----SerGlnSerTyrAlaThr 199
Qy 709 AAAACTGTATCATTAATGGAATTCAGATTAATATCAAAATGTACCTGCTGTATCGT 768
Db 200 ThrThrValThrAla-----ProProGlyGly----- 208
Qy 769 CCATTTATGATGCTTATATTCGTACAGATGTTAACCAATATCTTAGCATATACC 828
Db 209 -----ThrAlaThrValIlelleArgGluProProAsnTyrThr 221
Qy 829 AATGATTATACTTGTGTCGCGATCGTGCAGAGTAACCTTTCACCTTTAAGATGACT 888
Db 222 -----ValThrThrThrGluTyrTrpSerGlnSerTyrAlaThrThrThrIleThr 239
Qy 889 GGATACAAGATAGTAGTCCGGATCTAACGGTATTGTCAAT----- 930
Db 240 Ala-----ProProGlyGlyThrAspThrValIlelleArgGluProProAsnTyr 256
Qy 931 ---GTTGTCACTAGAACAGTTCACAGACAGTACCACTGCTGTCACACTTTTACCATT 987
Db 257 ThrValThrThrGluTyrTrpSerGlnSerTyrThrThrThrValThrGly 276
Qy 988 AATCAAGTGTGATAAACCAACAAATCGAATTTTGGCACTTATCCACCACTACC 1047
Db 277 ProProGly-----GlyThrAspThrValIlelleArgGluPro---ProAsnTyrThr 293
Qy 1048 ATCACAACT-----TCATATGTTGGTGTGACTACTTCTCTATCTGACT 1089
Db 294 ValThrThrThrGluTyrTrpSerGlnSerTyrAlaThrThr-----Thr 309
Qy 1090 AAGACTGCACCAATTTGGTGAACAGCTACTGTTATGTTGATGTCGCATATCATACATC 1149
Db 310 ValThrGlyProProGlyGlyThrAspThrValIlelleArgGluProProAsnTyrThr 329
Qy 1150 ACACTGTTACAGTGAATGACAGGAAACATATCATACCAACCACTCGTACCAATCCA 1209
Db 330 ValThrThrThrGluTyrTrpSerGlnSerTyrAlaThrThrThrValThrGlyPro 349
Qy 1210 ACTGATTCATTTGACACAGTGTGTACAAAGTTCCA 1245
Db 350 ProGlyGlyThrAspThrValIlelleArgGluPro 361
RESULT 15
US-08-325-267A-2
; Sequence 2, Application US/08325267A
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; Patent No. 5585271
; GENERAL INFORMATION:
; APPLICANT: WATARI, JUNJI
; APPLICANT: TAKATA, YOSHIHIRO
; APPLICANT: OGAWA, MASAHIRO
; APPLICANT: PENTTILA, MERJA
; APPLICANT: ONNELA, MAIJA-LEENA
; APPLICANT: KERANEN, SIRKKA
; TITLE OF INVENTION: YEAST AGGLUTINATION GENES AND YEAST
; TITLE OF INVENTION: CONTAINING THEM
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HWY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,267A
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP PCT/JP94/00290
; FILING DATE: 24-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 38871/1993
; FILING DATE: 26-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 2589-023-0XPCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 2:
; LENGTH: 1537 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-325-267A-2
Alignment Scores:
Pred. No.: 9,45e-08 Length: 1537
Score: 177.00 Matches: 112
Percent Similarity: 32.72% Conservative: 47
Best Local Similarity: 23.05% Mismatches: 181
Query Match: 7.71% Indels: 146
DB: 1 Gaps: 25
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Qy 58 AATTATGCTTTCAAAGGCCAGGA---TACCCAACTTGGAAATGCTGTTGGTGGTCC 114
Db 104 AsnTrpGlyCysValGlyMetGlyAlaCysSerAsnSerGlnGlyIleAlaTyrTrpSer 123
Qy 115 TTAGAT-----GTTACCACTGCCAATCCAGGGATACATTCCATTGAAATATG----- 162
Db 124 ThrAspLeuPheGlyPheTyrThrThrProThrAsnVal---ThrLeuGluMetThrGly 142
Qy 163 -----CCATGTGTGTTTAAATATATCTACTCTCAAA----- 192
Db 143 TyrPheLeuProGlnThrGlySerTyrThrPheLysPheAlaThrValAspAspSer 162
Qy 192 ----- 192
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Db 163 AlaIleLeuSerValGlyGlyAlaThrAlaPheAsnCysCysAlaGlnGlnProPro 182
QY 193 ---ACATCTGTTGATTTAACTGCGATGGTGTAA--- 225
Db 183 IleThrSerThrAsnPheThrIleAspGlyIleYsProTrpGlyGlySerLeuProPro 202
QY 226 -----TATGCTACTCTGCAATTTATTTCTGGTGAAGAATTCACAACTTTTCTACATTA 279
Db 203 AsnIleGluGlyThrValTyrMetTyrAlaGlyTyrTyrProMet----- 218
QY 280 ACATGTAAGTGAACGCGCTTGAATATCCATTAAGGCATTTGGTACA----- 330
Db 219 -----LysValValTyrSerAsnAlaValSerTrpGlyThrLeuProIle 233
QY 331 ---GTTACTTTACCAATTTGCAATGTTGGTGAACAGGTTTCATCAACTGATTTGGAA 387
Db 234 SerValThrLeuPro-----AspGlyThrThrValSerAspPheGlu 248
QY 388 GATTCTAAATGTTTTACTGCTGTGTACCAATACAGTCACATTAATGATGGTGATAAGAT 447
Db 249 Gly-----TyrValTyrSerPheAsp----- 256
QY 448 ATCTCAATGATGTTGATTTGAAAGTCAACCGTT---GATCCAAGTGCATATTTGTAT 504
Db 257 -----AspLeuSerGlnSerAsnCysThrValProAspProSerAsnTyrAla--- 272
QY 505 GCTTCCAGAGTTATGCCAAGTCTCAATAAGTCAACAATCTTTTGTGGCACCACAATGT 564
Db 273 ValSerThrThrThrThrThrThrGluProTrpThrGlyThrPheThrSerThr 292
QY 565 GAAATGTTTACACATCTGTTACAAATGGGTTCTCCAGTAGTAGACGGTGTGCTATT 624
Db 293 GluMetThrThrValThrGlyThrAsnGlyValProThrAspGluThrValIleValIle 312
QY 625 GATTGTCAAATATTGATATGTTGATATCAAAAAGGATTAATGATGGAAATATCCGGTT 684
Db 313 ArgThrProThrThrAlaSerThrIleThrThrThrGluProTrpAsnSerThrPhe 332
QY 685 TCATCTGAATCAATTTAGTTACACTTAAACCTGATCACTAATGCAATTCAGATTAAATAT 744
Db 333 ThrSerThrSerThrGluLeuThrValThrGlyThrAsnGlyValArgThrAspGlu 352
QY 745 CAAATGTACCTGCTGTTATCGTCCATTTATTGATGCTTATATTCTCTGACAGATGTT 804
Db 353 ThrIleIle-----ValIleArgThrProThrThrAlaThrThrAla 366
QY 805 AACCAATATATTAGCATATACCAATGATATATCTTGTGCTGGCAGTCTCTGCAAGT 864
Db 367 IleThrThrThrGluProTrpAsnSerThrPheThrSerThrSerThrGluLeu----- 384
QY 865 AAACCTTTCTACTTTAAGATGGACTGATACAAGAATAGTATGCCGATCTAACGGTATT 924
Db 385 -----ThrThrValThrGlyThrAsnGlyLeu 393
QY 925 -----GTCAATGTTGTACAACTAGAACAGTTACAGACAGTACCACTGCTGCTCACT 975
Db 394 ProThrAspGluThrIleIleValIleArgThrProThrThrAlaThrAlaMetThr 413
QY 976 ACTTTA---CCATTCAATCCAGTGTGATAAACCAAAACA----- 1014
Db 414 ThrThrGlnProTrpAsnAspThrPheThrSerThrSerThrGluMetThrThrValThr 433
QY 1015 -----ATCGAAATTTTGCACACCTATTTCACACC 1041
Db 434 GlyThrAsnGlyLeuProThrAspGluThrIleIleValIleArgThrProThrThrAla 453
QY 1042 ACTACCATCACACT-----TCATATGTTGGTGTGACTACTTCC 1080
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QY 1081 TATCTGACTAAGACTGCA-----CCATTTGGTGAACAGCTACTGTTATTGTT 1128
Db 474 MetThrThrValThrGlyThrAsnGlyLeuProThrAspGluThr-----IleIleValIle 492

QY 1129 GATGTGCCATATCATACTACCACA-----ACTGTTACCAGTGAATGGACAGGAACAATC 1182
Db 493 ArgThrProThrThrAlaThrThrAlaMetThrThrThrGlnProTrpAsnAspThrPhe 512
QY 1183 ACT-----ACCACCACAACCTCGTACCAAT-----CCAAGTGAATTC 1218
Db 513 ThrSerThrSerThrGluMetThrThrValThrGlyThrAsnGlyLeuProThrAsp--- 531
QY 1219 ATTGACACAGTGGTGTA 1236
Db 532 ---GluThrIleIleVal 536

Search completed: September 8, 2005, 17:52:35
Job time : 60.5 secs


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QY 181 ACTACTTCACAAACATCTGTTGATTTAACTGCCGATGCTGTTAAATATGCTACTGTCAA 240
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QY 78 ThrThrSerGlnThrSerValAspLeuThrAlaAspGlyValIysTyrAlaThrCysGln 97
Db |||||||
QY 241 TTTTATTCTGGTGAAGAATTCACAACTTTTTTCTACATTAACATGTAAGTGAACGACGCT 300
Db |||||||
QY 98 PheTyrSerGlyGluGluPheThrThrPheSerThrLeuThrCysThrValAsnAspAla 117
Db |||||||
QY 301 TTGAATCATCCATTAAAGGATTTGGTACAGTTACTTACCAATTGCAATTCATTTGGT 360
Db |||||||
QY 118 LeuIysSerSerIleLysAlaPheGlyThrValThrLeuProIleAlaPheAsnValGly 137
Db |||||||
QY 361 GGAACAGTTTCATCAACTGATTTGGAAGATTCCTAAATGTTTAACTGCTGGTACCAATACA 420
Db |||||||
QY 138 GlyThrGlySerThrAspLeuGluAspSerLysCysPheThrAlaGlyThrAsnThr 157
Db |||||||
QY 421 GTCACATTTAATGATGGTGATAAGATATCTCAATTGATGTTGAGTTGAAAAAGTCAACC 480
Db |||||||
QY 158 ValThrPheAsnAspGlyAspLysAspIleSerIleAspValGluPheGluLysSerThr 177
Db |||||||
QY 481 GTTGATCCAAGTGCATATTTGATGCTTCCAGAGTTATGCAAGTCTCATATAGGTACA 540
Db |||||||
QY 178 ValAspProSerAlaTyrLeuTyrAlaSerArgValMetProSerLeuAsnLysValThr 197
Db |||||||
QY 541 ACTCTTTTGTGGCACCACCAATGTGAAAATGGTTTACACATCTGATCAATGGGGTCTCC 600
Db |||||||
QY 198 ThrLeuPheValAlaProGlnCysGluAsnGlyTyrThrSerGlyThrMetGlyPheSer 217
Db |||||||
QY 601 AGTAGTAACGGTGCATTTGATTTGATTTGCTCAAAATATTCATATGATGATACAAAGGA 660
Db |||||||
QY 218 SerSerAsnGlyAspValAlaIleAspCysSerAsnIleHisIleGlyIleThrLysGly 237
Db |||||||
QY 661 TTAATGATGGAATTAATCCGGTTTCATCTGAATCATTTAGTTACACTAAACTGTGACA 720
Db |||||||
QY 238 LeuAsnAspTrpAsnTyrProValSerSerGluSerPheSerTyrThrLysThrCysThr 257
Db |||||||
QY 721 TCTAATCGAATTCAGATTAATAATCAAAATGTACTCTGCTGATTCCTCCATTTATTGAT 780
Db |||||||
QY 258 SerAsnGlyIleGlnIleLysTyrGlnAsnValProIleGlyTyrArgProPheIleAsp 277
Db |||||||
QY 781 GCTTATATTCTGTACAGATGTTAACCAATATATCTTTAGCATATACCAATGATTATACT 840
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QY 278 AlaTyrIleSerAlaThrAspValAsnGlnTyrThrLeuAlaTyrThrAsnAspTyrThr 297
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QY 841 TGTCTGGCAGTCTGTCGAAGTAAACCTTTTCACTTTTAAGATGGAGCTGGATACAGAAT 900
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QY 298 CysAlaGlySerArgLeuGlnSerLysProPheThrLeuArgTrpThrGlyTyrLysAsn 317
Db |||||||
QY 901 AGTCATGCCGATCTAACGGTATTGTCATTTGTTGCTACAACTAGAAACAGTTACAGACAGT 960
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QY 318 SerAspAlaGlySerAsnGlyIleValIleValAlaThrThrArgThrValThrAspSer 337
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QY 961 ACCACTGCTGCTACTTTACCATTCATCCAAAGTGTGATATAAAACCAAAACATCGAA 1020
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QY 1021 ATTTTGCACCTATTCCAAACCACTACCATTCACACTTCATATGTTGGTGGTACTTCC 1080
Db |||||||
QY 358 IleLeuGlnProIleProThrThrThrIleThrThrSerTyrValGlyValThrThrSer 377
Db |||||||
QY 1081 TATCTGATAGACTGACCAAAATTTGGTGAACACACTACTGTTATTTGTTGATGTGCCATAT 1140
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QY 378 TyrLeuThrLysThrAlaProIleGlyGluThrAlaThrValIleValAspValProTyr 397
Db |||||||
QY 1141 CATACTACCAACTGTTTACAGTGAATGGACAGGAACATTCATCACTACCAACACTCGT 1200
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QY 398 HisThrThrThrThrValThrSerGluTrpThrGlyThrIleThrThrThrThrArg 417
Db |||||||
QY 1201 ACCAATCCAACTGATTCAAATTTGACACAGTGGTGTACAAAGTTCCA 1245
Db |||||||
QY 418 ThrAsnProThrAspSerIleAspThrValValGlnValPro 432
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RESULT 2

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T30531
agglutinin-like adhesin - Yeast (Candida albicans)
C;Species: Candida albicans
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30531
R;Gaur, N.K.; Klotz, S.A.
Infect. Immun. 65, 5289-5294, 1997
A;Title: Expression, cloning, and characterization of a Candida albicans gene, ALA1, th
A;Reference number: Z20847; UID:98053977; PMID:9393828
A;Accession: T30531
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1419 <GAU>
A;Cross-references: UNIPROT:O13368; EMBL:AF025429; NID:92522218; PID:92522219; PIDN:AA
C;Genetics:
A;Gene: ALA1
C;Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase
Alignment Scores: 6.51e-137 Length: 1419
Pred. No.: 1903.00 Matches: 358
Score: 91.33% Conservative: 21
Percent Similarity: 86.27% Mismatches: 36
Best Local Similarity: 82.85% Indels: 0
Query Match: 2 Gaps: 0
DB:
US-09-715-876-7_COPY_52_1296 (1-1245) x T30531 (1-1419)
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QY 1 AGACAATCACCTGGTGTGTTTGAATGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 60
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QY 18 LysAlaIleThrGlyIlePheAsnSerIleAspSerLeuThrTrpSerAsnAlaGlyAsn 37
Db |||||||
QY 61 TATGCTTTCAAAGGGCCAGATACCCAACTTGGAATGCTGTTTGGTGGTGGTGGTGGTGGTGGTGG 120
Db |||||||
QY 38 TyrAlaPheLysGlyProGlyTyrProThrTrpAsnAlaValLeuGlyTrpSerLeuAsp 57
Db |||||||
QY 121 GGTACACAGTCCCAATCCAGGGATACATTCACATTTGAATATGCAATGCTGTTGTTAAATAT 180
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QY 58 GlyThrSerAlaAsnProGlyAspThrPheIleLeuAsnMetProCysValPheLysPhe 77
Db |||||||
QY 181 ACTACTTCACAAACATCTGTTGATTTAACTGCCGATGCTGTTAAATATGCTACTTCTCAA 240
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Db |||||||
QY 241 TTTTATTCTGGTGAAGAATTCACAACTTTTTTCTACATTAACATGTAAGTGAACGACGCT 300
Db |||||||
QY 98 PheTyrSerGlyGluGluPheThrThrPheSerSerLeuLysCysThrValAsnAsn 117
Db |||||||
QY 301 TTGAATCATCCATTAAAGGATTTGGTACAGTTACTTTCACCAATTCATTCATTCATTCATTCAT 360
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QY 118 LeuArgSerSerIleLysAlaLeuGlyThrValThrLeuProIleAlaPheAsnValGly 137
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QY 361 GGAACAGTTTCATCAACTGATTTGGAAGATTCCTAAATGTTTAACTGCTGGTACCAATACA 420
Db |||||||
QY 138 GlyThrGlySerValAspLeuGluAspSerLysCysPheThrAlaGlyThrAsnThr 157
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QY 421 GTCACATTTAATGATGGTGATAAGATATCTCAATTGATGTTGAGTTGAAAAAGTCAACC 480
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QY 481 GTTGATCCAAGTGCATATTTGATGCTCCAGAGTTATGCAAGTCTCATATAGGTACA 540
Db |||||||
QY 178 ValAspGlnSerGlyTyrLeuThrThrSerArgPheMetProSerLeuAsnLysIleAla 197
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submitted to the EMBL Data Library, February 1994

A;Description: Sequencing of chromosome I of *Saccharomyces cerevisiae*: analysis of the 5

A;Reference number: S53458

A;Accession: S53465

A;Molecule type: DNA

A;Residues: 1-1537 -BUS>

A;Cross-references: UNIPROT:P32768; EMBL:L28920; NID:g1616966; PIDN:AAC09499.1; PID:G694

R;Watarai, J.; Takata, Y.; Ogawa, M.; Sahara, H.; Koshino, S.; Onnaja, M.L.; Airaksinen,

Yeast 10, 211-225, 1994

A;Title: Molecular cloning and analysis of the yeast flocculation gene FLO1.

A;Reference number: S43543; MUID:94262325; PMID:8203162

A;Accession: S43543

A;Molecule type: DNA

A;Residues: 1-428; 'M', 430-473, 'M', 475-518, 'M', 520-549, 'T', 551-608, 'L', 610-636, 'M', 638-659

A;Cross-references: EMBL:X78160

K;Onnella, M.
submitted to the EMBL Data Library, September 1994
A:Reference number: S57851
A:Accession: S57851
A:Molecule type: DNA
A:Residues: 1-428, 'M', 430-463, 'D', 465-473, 'M', 475-518, 'M', 520-549, 'T', 551-608, 'L', 610-632
A:Cross-references: EMBL:X78160; MID:G535933; FIDN:CAA55024.1; FID:G535934
R:Teunissen, A.W.R.H.; Holub, E.; van der Hucht, J.; van den Berg, J.A.; Steensma, H.Y.
Yeast 9, 423-427, 1993
A:Title: Sequence of the open reading frame of the FLO1 gene from *Saccharomyces cerevisiae*
A:Reference number: S31230; MUID:93289821; PMID:8511970
A:Accession: S31230
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-296, 927-1516, 'TAYWPVVV' <TEU>
R:Bidard, F.; Bonny, M.; Blondin, B.; Dequin, S.; Barre, P.
Yeast 11, 809-822, 1995
A:Title: The *Saccharomyces cerevisiae* FLO1 flocculation gene encodes for a cell surface
A:Reference number: S57349; MUID:96090130; PMID:7483845
A:Accession: S57349
A:Molecule type: DNA
A:Residues: 1243-1274; 1308-1339; 1359-1390 <BID>
C:Genetics:
A:Gene: SGD:FLO1
A:Cross-references: SGD:S0000084; MIPS:YAR050W
A:Map position: 1R
C:Keywords: duplication; glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-1537/Product: flocculation protein FLO1 #status predicted <MAT>
F:953-997/Domain: repeat A2 <RA2>
F:998-1042/Domain: repeat A3 <RA3>
F:1043-1081/Domain: repeat A4 <RA4>
F:1226-1276/Domain: repeat B1 <RB1>
F:1277-1284/Domain: repeat B2 (partial) #status atypical <RB2>
F:1291-1341/Domain: repeat B3 <RB3>
F:1342-1392/Domain: repeat B4 <RB4>
F:1408-1416/Domain: repeat C1 <RC1>
F:1417-1425/Domain: repeat C2 <RC2>
F:1426-1434/Domain: repeat C3 <RC3>
F:135-187-262-1114/Binding site: carbohydrate (Asn) (covalent) #status predicted

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Alignment Scores:
Pred. No.:      1.35e-05      Length:      1537
Score:          177.00      Matches:      112
Percent Similarity: 32.72%      Conservative: 47
Best Local Similarity: 23.05%      Mismatches:  181
Query Match:      7.71%      Indels:      146
DB:              2      Gaps:      25

US-09-715-876-7_COPY_52_1296 (1-1245) x S53465 (1-1537)

Qy  58  AATTATGCTTTCAAAGGCCCAGGA---TACCRAACTTGGGAATGCTGTTTGGGTGGTGCC 114
    |||:::  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db  104  AsnTrpGlyCysLysGlyMetGlyAlaCysSerAsnSerGlnGlyIleAlaTyTrpSer 123
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy  115  TTAGAT-----GGTACAGTGGCCCAATCCAGGGGATACATTTCACATTGAATATG----- 162
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db  124  ThrAspLeuPheGlyPheTyTrThrProThrAsnVal---ThrLeuGluMetThrGly 142
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C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31113
R;Barnes, D.A.; Bonnin, A.; Huang, J.X.; Gousset, L.; Wu, J.; Gut, J.; Doyle, P.; Dubremet
Mol. Biochem. Parasitol. 95, 93-110, 1998
A;Title: A novel multi-domain mucin-like glycoprotein of *Cryptosporidium parvum* mediates
A;Reference number: Z20989; MUID:99066935; PMID:9851610
A;Accession: T31113
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-1832 <BAR>
A;Cross-references: UNIPROT:O96503; EMBL:AF068065; NID:94063041; PID:94063042; PIDN:AAAC9

Alignment Scores:		
Pred. No.:	1.77e-05	Length:
Score:	175.50	Matches:
Percent Similarity:	33.9%	Conservative:
Best Local Similarity:	22.8%	Mismatches:
Query Match:	7.64%	Indels:
DB:	2	Gaps:

US-09-715-876-7 COPY 52 1296 (1-1245) x T31113 (1-1832)

[illegible]

RESULT 9

T40778
hypothetical 129.5 kd protein - fission yeast (*Schizosaccharomyces pombe*)
C:Species: *Schizosaccharomyces pombe*
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T40778
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C.M.
submitted to the EMBL Data Library, February 1998
A;Reference number: Z21884
A;Accession: T40778
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-973 <LYN>
A;Cross-references: EMBL:AL021837; PIDN:CAA17032.1; GSPDB:GN00067; SPDB:SPBC947.04
A;Experimental source: strain 972h-; cosmid c947
C;Genetics:
A;Gene: SPDB:SPBC947.04
A;Map position: 2

Alignment Scores:	
Pred. No.:	2,02e-05
Score:	174.50
Percent Similarity:	35.33%
Best Local Similarity:	22.63%
Query Match:	7.60%
DR:	2
Length:	973
Matches:	112
Conservative:	63
Mismatches:	157
Indels:	163
Gaps:	25

US-09-715-876-7 COPY 52 1296 (1-1245) X T40778 (1-973)

Qy	40	ACTTGGTC	CAATGCTGCTAAATTATGCTTTTCAAAGGCCGAGGATACCCAACTTGGGAATGCT	99
Dd	149	ThrTrpSerThrAsnLeu	-----ProThrAsnProThrThrThrAla	162
Qy	100	GTTTGGTG	TGGTCCTTAGATGGTACCAGTGCCCAATCCAGGGATACATTCACATGTAAT	159
Dd	163	Ile-----TyrSerThrSerGlySerSer	-----AsnIleThr	173
Qy	160	ATGCATGTG	TGTTAAATAATACTACTTCAACAACATCTGTT---GATTTAACTGCCGAT	216
Dd	174	ThrProTyrSerAsnAspIleThrAsnSerValAsnAspIleThrSerLys	193	

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Qy 217 -----GGTGTAAATATGCTACTTGTGTCATTTTATTCTGCTGAAGAATTC----- 261
Db 194 TyrLeuSerValGlyThrIleThrLeuThrThrIleSerGlySerAspLeuThrThrSer 213
Qy 262 -----ACAACTTTTCTCATTTAACATGACTGCTG----- 291
Db 214 ThrPheProAlaAsnGlyThrThrSerGlyThrValGluValValIleProThrAlaGly 233
Qy 292 -----AACGACGCTTTGAATCATTCATTAAGCGATTT 324
Db 234 ThrValThrGluThrAlaValSerGlySerGluLeuThrThrSerThrPheProAlaAsn 253
Qy 325 GGTACAGTT-----ACTTTACCAATTCATTCATTTGCTGGAACAGGTTTCATCAACT 378
Db 254 GlyThrThrSerGlyThrValGluValValIleProThrAlaGlyThrArgThrValThr 273
Qy 379 GATTTGGAAGATTCATAATGTTTT----- 402
Db 274 LysIleSerGlySerLysPhePheThrThrThrThrAspAlaSerGlyThrValSerGly 293
Qy 403 -----ACTGCTGTTACCAATACAGTCACATTTAATGATGGTAT 441
Db 294 ThrValGluValValLeuProThrAlaGlyThrAsnThrMetThrValValSerGlySer 313
Qy 442 AAA-----GATATCTCAATTGATGTTGAGTTTGAAGTCAACGGTT 483
Db 314 ArgPhePheThrSerValValSerAlaSerGlyThrValSerGlyGluGlnValIleVal 333
Qy 484 GATCCAAGTGCATATTTGTATGCTTCCAGA----- 513
Db 334 TyrProThrAlaGlyMetValThrGluThrIleValSerGlySerGluIlePheAsnThr 353
Qy 514 -----GTTATGCCAAGTCTCAAT 531
Db 354 ThrTyrProAlaSerGlyThrArgThrGlyThrValGluValValIleProThrAlaGly 373
Qy 532 AAGTTCACA-----ACTCTTTTGTGGCACCACATGTCGAAAT 570
Db 374 ThrValThrGluThrGluIleSerGlySerGlyLeuLeuThrThrSerThrPheProAlaAsn 393
Qy 571 GGTACACATCTGGTACATGCGGGTCTCCAGTAGTAACGGTGACGTTGCTATTGATTGC 630
Db 394 GlyThrThrSerGlyThrVal-----GluValValIleProThr 406
Qy 631 TCAAAATATTCATTTGGTATCACAAAGATTAATGATGGAATTCGCGTTTCATCT 690
Db 407 AlaGlyThrArgThr---ValThrLys-----IleSerGly 417
Qy 691 GAATCATTTAGTTACACTAAACTTGTACATCTAATGGAATTCAGATTAAATACAAAT 750
Db 418 SerLysPhe---PheThrThrThrThrAspAlaSerGlyThr----- 430
Qy 751 GPACCTGCTGTTATGCTCAATTTATGATGCTTATATTCTGCTACAGATGTTAAACCA 810
Db 431 -----ValSerGlyThrValGluValVal 438
Qy 811 TATACTTTAGCATATACCAATGATTATACT---TGTGCTGGCAGTCGCTCGCAAGTAAA 867
Db 439 LeuProThrAlaGlyThrAsnThrMetThrValValSerGlySerArgPhe----- 455
Qy 868 CTTTCACATTTAAGATGGACTGGATACAGAATAGTAGTCGCGGATCTAACGGT----- 921
Db 456 -----PheThrSerValValSerAlaSerGlyThrValSerGlyGluHis 470
Qy 922 ATTGTCAATTTGCTACACTAGAACAGTTACAGACAGTACCACCTGCT----- 969
Db 471 IleIleValGluProThrAlaGlyValValThrGluThrValValSerGlySerValGly 490
Qy 970 ---GTCACCTACTTTTACCAATTCATTCAGTGTGTGATAAAACCAACCAATGGAATTTTG 1026
Db 491 TyrThrThrThrThrTyrProAlaHisAspThrVal-----SerGlyThrValGluValVal 508
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Qy 1027 CAACCT-----ATTCCAACACCACTACCATCAACAATTCATATGTTGGTGTGACTACT 1077
Db 509 GluProThrAlaGlyValValThrGluThrValSerGlySerValGlyThrThrThr 528
Qy 1078 TCCTATCTGACTAAGACTGCACCAATTTGGTGAACACAGCTACTGTTATTGTTGATGTGCCA 1137
Db 529 AlaTyr-----ProAlaHisAspThrValSerGlyThrValGluValVal 543
Qy 1138 TATCATACT-----ACCACAACCTGTTTACCAGTGAATGGACAGCAACAATCACT 1185
Db 544 GluProThrAlaGlyValValThrGluThrValValSerGlySerValGlyThrThrThr 563
Qy 1186 ACCACCACAACCTGTCACCAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCC 1230
Db 564 ThrTyrProAlaHisAspThrValSerGlyThrValGluValValVal 578
RESULT 10
T38221
hypothetical serine-threonine rich protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 17-Nov-2000
C:Accession: T38221
R:Murphy, D.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, February 1998
A:Reference number: Z21780
A:Accession: T38221
A:Molecule type: DNA
A:Residues: 1-456 <MUR>
A:Cross-references: EMBL:AL021813; PIDN:CAAL6975.1; GSPDB:GN00066; SPDB:SPAC23A1.01c
A:Experimental source: strain 972h; cosmid c23A1
C:Genetics:
A:Gene: SPDB:SPAC23A1.01c
A:Map position: 1
C:Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase
Alignment Scores:
Pred. No.: 3,22e-05 Length: 456
Score: 171.50 Matches: 110
Percent Similarity: 37.70% Conservative: 57
Best Local Similarity: 24.83% Mismatches: 147
Query Match: 7.47% Indels: 129
DB: 2 Gaps: 24
US-09-715-876-7_copy_52_1296 (1-1245) x T38221 (1-456)
Qy 25 AGTTTAAATTCATTAATCTGTCCTCAATGCTGCTAATTAATTAATTAATTAATTAATTAATTAAT 84
Db 94 SerPheThrSerIleArg---AspAspSerValIleTyrAlaGlnSerGlyThrPheTyr 112
Qy 85 CCAACTTGGAAATGCTGTTTGGGTTGCTCTTAGATGTCACGTCACCAATCCAGGGAT 144
Db 113 -----IleValGlyGly-----GluGlyIleSerSerThrThrGlySer 125
Qy 145 ACATTCACATTTGAATATGCCATGCTGTTTAAATATATACTACTTCCACAA----- 192
Db 126 ThrPhe-----GlnSerMetThrThrPheThrSerSerGlnThrAsnSerGly 141
Qy 193 -----ACATCTGTTGATTTAACTCCGCGATGGTGT 222
Db 142 HisAlaSerAlaSerThrSerIleProSerThrAlaIleThrValThrAlaAsnSerThr 161
Qy 223 AAATAT-----GCTACTTGTCAATTT---TATTCTGCTGGAAGAATTCACAACTTTTCT 273
Db 162 IleTyrSerSerAlaThrSerSerPheProTyrSer-----ThrAspValSer 177
Qy 274 ACATTAACATGACTACTGTGAACAGCGCTTTG-----AAATCATCCATTAAAG 318
Db 178 ValSerThrGlyThrSerThrAspIleValThrLeuProProAlaSerSerThrSer 197
Qy 319 GCATTTGGTACAGTTACTTTTACCAATTCATTCATGTTGTTGGTGGACAGGTTTCATCACT 378
Db 198 SerPheSerThrIleThr-----AsnThrSer 206
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Db 381 Phe-----AspSerSerIleSerGlyThr-----Lys 389
QY 883 TGGACTGATACAGATAGATGATGCGGATCTAACGGTATTGTCATTTGCTACAACT 942
Db 390 TrpCysPheTyrSerThrSerGln-----ValAlaAlaThr 401
QY 943 AGAACAGTTACAGACAGPACCACTGCTGCTACTACTTTTACCAATCAATCCAAAGTTGAT 1002
Db 402 LysThrThrThrThrThrThrThr-----ThrThrThrThrThrThrThrThr 419
QY 1003 AAA-----ACCAAAACAATCGAAATTTGGCAACTATTCGAAGTGGTGA 1110
Db 420 LysAlaThrThrThrThrThrThrThr-----ThrThrThrThrThrThrThrThr 439
QY 1051 ACAACTTCATATGTTGGTGTGACTACTTCCTATCTGCTAAGACTGACCAATTTGGTGA 1110
Db 440 ThrThrThr-----ThrLysAlaThrThrThrThrThrThrThrThrThrThrThrThr 458
QY 1111 ACAGTACTGTTATTTGTTGATGTGCCATATCATCTACTACCAACTGTTTACCAGTGAATGG 1170
Db 459 ThrThrLysAlaThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 478
QY 1171 ACAGGAACAATCACTACC-----ACCACAACCTGTCACCAATCCAACTGATTCAAATTCAC 1224
Db 479 ThrLysAlaThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 498
QY 1225 ACAGTGGTGGTACAAAGTTCCA 1245
Db 499 LysAlaThrThrThrThrPro 505

RESULT 12
T22808
hypochemical protein F56H9.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22808
R:Burton, J.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19618
A:Accession: T22808
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-770 <WIL>
A:Cross-references: UNIPROT:Q20908; EMBL:Z74473; PIDN:CAA98949.1; GSPDB:GN00023; CESP:FS
A:Experimental source: clone F56H9
C:Genetics:
A:Gene: CESP:F56H9.1
A:Map position: 5
A:Introns: 235/1; 262/2; 320/1; 367/2; 510/3; 654/1; 681/2

Alignment Scores:
Pred. No.: 0.000125 Length: 770
Score: 164.00 Matches: 104
Percent Similarity: 35.60% Conservative: 58
Best Local Similarity: 22.86% Mismatches: 144
Query Match: 7.14% Indels: 149
DB: 2 Gaps: 20

US-09-715-876-7_COPY_52_1296 (1-1245) x T22808 (1-770)
QY 16 GTTTTGTAGTTTAAATTCATTAACCTGGTCCAAATGCTGCTCAATATGCTTTCAAGGG 75
Db 295 IlePheAspValPheAsn-----GlnProAlaGluAsnGlnGlyPhe----- 308
QY 76 CCAGGATACCACTGGAACTGCTGTTTGGTGGTCTTGGTGGTCTTAGATGGTACCAGTGCCAA 135
Db 309 ProGlnSerValThrValAsnAlaGlnCys----- 318
QY 136 CCAGGGGATACATTCACATATGCAATATGCAATGCTGTTGTTAAATATACCTACTTCAACA 195
Db 319 -----AsnArgIleLeuIleAsnLeuPheMetPhePheLysPhe----- 331
QY 196 TCTGTTGATTTAACTGCCGATGGTGTAAATATGCTACTGTCTCAATTTATTTCTGGTGA 255
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Db 332 -----LeuSerTyrGluLysThrSerPheTyr----- 340
QY 256 GAATTCACAATTTTCTACATTAACATGTACTGTGACACCGCTTTGAATCATCATTCAT 315
Db 341 -----IleLeuCyseThrSerLys-ThrLeuSerAsnPheIleLe 353
QY 316 AAGGCATTTG-----GTACAGTTACTTTTAC-----CAATTGCAATTC 351
Db 353 uLeuThrValTyrPheLeuTyrIleGlyProThrGluLeuLeuTyrThrGlnIleGlySe 373
QY 352 AATG-----TTGGTGGGAACA 366
Db 373 rMetAsnLeuAsnThrTyrLeuAsnGlnThrMetGlyLeuGlyMetTyrLeuGlnGlyPr 393
QY 367 GGTTCATCACTGATTTGGAAGATTTCTAATGTTTACTGCTG----- 409
Db 393 oIleThrGlnMetIleThrIleAsnArgPheLeuValIleThrPheThrProThrHi 413
QY 410 -GTACCAATACAGTCACATTTAATGATGGTG-----ATAAGATATCTCAATTTGATGTT 462
Db 413 sValProGlnTyrSerHisArgIleThrLeuGlyAlaLeuSerValSerTrpIleThrVa 433
QY 463 GAGTTTGAAAGTCAACCGTTGATCCAAAGTGCATATTTGTATGCTTCCAGAGTTA----- 517
Db 433 lThrTrpLeuSerThr-----LeuIleGlyLeuProGlyPheAspAs 447
QY 518 -----TGCCAAGTCTCAATAGGTCACA 540
Db 447 nAsnAsnAsnPheAspIleIleAsnLeuAlaAsnCysArgValProIleGlyPheGl 467
QY 541 ACTCTTTTCTGGCACCACACAATGTGAAATGGTTACACATCTGTGACAAATGGGTTCTCC 600
Db 467 u-----HisIleGlyTyrTyrSerThrPr 475
QY 601 AGTAGTAACG---GTGACGTTGCTATTGATTTGCTCAAATATTCATATTTGGTATCACAAA 657
Db 475 oCysAsnAsnGlnIleThrIleIleValSerGlyIlePhe----- 489
QY 658 GGAATTAATGATTTGGAATATTCGGTTTCATCTGATCATTCATTTAGTTACATAAACTTGT 717
Db 490 -----LeuIleGlyPheLeuThrAsnPheMetAsnPheMetIleGlyGlyLysLeuIl 507
QY 718 ACAT-----CTAATGGAATTCAGATTAATAATACAA-----AT 750
Db 507 eTyrThrTrpLysThrLeuThrIlePheArgPheLeuSerAsnPheLysCysValMetLy 527
QY 751 GTACCTGCTGCTTATCGTCATTTTATGATGCTTATATTTCTGCTCAGAGATGTTAAACCA 810
Db 527 sTrpIleSerThrLeuLeuHisIleLeuLeuLeuThrTyrLysLeu--AspValIleAsn 546
QY 811 TATACCTTTAGCATATACCAATGATATATCTTGTGCTGCGAGTCTGCTGCAAGTAAACCT 870
Db 547 -----SerCysIleAlaThrSerProThrAlaAspPro 557
QY 871 TTCATTTTAAGATGGACTGGATACAGAAATAGTATGATCGCGATCTAACGGTATTGTCTATT 930
Db 558 ThrThr-----ThrThrThrGluAlaThrThrThrThrGluIle 570
QY 931 GTTGCTACAACCTAGAACAGTTTACAGACAGTACCACTGCTGCTCACTACTTTTACCATTCAAT 990
Db 571 ThrThrThrThrGluGluValThrThrThrThrGluProValThrThrThrThrThrPro 590
QY 991 CCAAGTGTGTATAAAACCAAAACAATCGAAATTTTGGCAACTATTCACCACTACCAATC 1050
Db 591 ThrThrThrSerThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 610
QY 1051 ACAACTTCATATGTTGGTGTGACTACTTCTCTGATCTGATAGCTGACCACTGCAATTTGGTGA 1110
Db 611 ThrProThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 630
QY 1111 ACAGCTACTGTTATTTGTTGATGTGCCATATCATCTACTACCACTGTTTACCAGTGAATGG 1170
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Db 631 ThrSerThr-----ThrThrThrThrThrThrThrThrThr 642

Qy 1171 ACAGGAACAATCACTACCACCAACACTCGTACCAATCCA 1209

Db 643 ThrAlaThrProThrThrThrThrThrThrThrMetProPro 655

RESULT 13

S48992

floculation protein homolog YHR211w - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C:Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004

C:Accession: S48992

R:Macri, C.

submitted to the EMBL Data Library, February 1994

A:Description: The sequence of S. cerevisiae cosmid 9177.

A:Reference number: S46671

A:Accession: S48992

A:Molecule type: DNA

A:Residues: 1-1075 <MAC>

A:Cross-references: UNIPROT:P38894; EMBL:U00029; NID:G551322; PID:G458919; GSPDB:GN00008

C:Genetics:

A:Gene: SGD:FLO5; MIPS:YHR211w

A:Cross-references: SGD:S0001254

A:Map position: 8R

Alignment Scores:

Pred. No.:	0.000198	Length:	1075
Score:	161.50	Matches:	110
Percent Similarity:	33.74%	Conservative:	57
Best Local Similarity:	22.22%	Mismatches:	209
Query Match:	7.03%	Indels:	119
DB:	2	Gaps:	22

US-09-715-876-7_COPY_52_1296 (1-1245) x S48992 (1-1075)

Qy 58 AATTATGCTTTCAAGGCCAGGA---TACCACACTTGGAAATGCTGTTGGGTGGTGC 114

Db 104 AsnTrpGlyCysLysGlyMetGlyAlaCysSerAsnSerGlnGlyIleAlaTyrTrpSer 123

Qy 115 TTAGAT-----GGTACCAGTCCCAATCCAGGGATACATTCACATTGAATATG- 162

Db 124 ThrAspLeuPheGlyPheTyrThrThrProThrAsnVal---ThrLeuGluMetThrGly 142

Qy 163 -----CCATGTGTGTTTAAATATATCTACTTTCACAAACATCTGTTGATTTAACT 210

Lb 143 TyrPheLeuProGlnThrGlySerTyrThrPheSerPheAlaThrValAspAspSer 162

Qy 211 GCC-----GATGGTGTAAATATGCTACTTGTCTCAATTTATCTGGTGAA 255

Db 163 AlaIleLeuSerValGlyGlySerIleAlaPheGluCysCys-----AlaGln 178

Qy 256 GAATTTCACAACTTTTCTACATTAAACATGCTACTGTGAAC----- 294

Db 179 GluGlnProIleThrSerThrAsnPheThrIleAsnGlyIleLysProTrpAspGly 198

Qy 294 ----- 294

Db 199 SerLeuProAspAsnIleThrGlyThrValTyrMetTyrAlaGlyTyrTyrProLeu 218

Qy 295 GACGCTTGAATCATCCATTAAAGCAATTTGGTACAGTTACTTTACCAATTCATCAAT 354

Db 219 LysValValTyrSerAsnAlaValSerTrpGlyThrLeuProIleSerValGluLeuPro 238

Qy 355 GTTGGTGGACAGGTTTCATCAACT-----GATTGTG 384

Db 239 AspGlyThrThrValSerAspAsnPheGluGlyTyrValTyrSerPheAspAspAspLeu 258

Qy 385 GAAGATTCTTAATGT-----TTTACTGCTGGTACCAATACATACAGTC 423

Db 259 SerGlnSerAsnCysThrIleProAspProSerIleHisThrThrSerThrIleThrThr 278

Qy 424 -----ACATTTAATGATGCTGATATAAGATATCTCAATTGATGT 462

Db 279 ThrThrGluProTrpThrGlyThrPheThrSerThrSerThrGluMetThrThrIleThr 298

Qy 463 GAGTTTGAAGAAAGTCAACCGTGTGATCCAAAGTGCATATTTGTAT-----GCT 507

Db 299 AspThrAsnGlyGlnLeuThrAspGluThrValIleValIleArgThrProThrAla 318

Qy 508 TCCAGAGTTATGCAAGTCTCAATAAGGTACACACTCTTTTGTGGCACCACACATGTGA 567

Db 319 SerThrIleThrThrThrGluProTrpThrGlyThrPheThrSerThrSerThrGlu 338

Qy 568 AATGGTTACACATCTCGTACAAATGGGTTCTCCAGTAGTAACCGTGCAGTGTGCTATTGAT 627

Db 339 MetThrThrValThrGlyThrAsnGlyGlnProThrAspGluThrValIleValIleArg 358

Qy 628 TGCTCAAAATATTCATATTCGTATACAAAAGGATTAATGAATTCGGATTAATCCGGTTTCA 687

Db 359 ThrProThrSerGluGlyLeuIleThrThrThrGluProTrpThrGlyThrPheThr 378

Qy 688 TCTGAATCATTTAGTTACACTAAACTTGTACATCTAATGAATTCAGATTAATATCA 747

Db 379 SerThrSerThrGluMetThrThrValThrGlyThrAsnGly---GlnProThrAspGlu 397

Qy 748 AATGTACTCTGCTGTTATCGTCCATTTATGATGCTTATATATTTCTGCTACAGATGTTAAC 807

Db 398 ThrValIleValIleArgThrProThrSerGluGlyLeuIleThrThrThr 414

Qy 808 CAATATACATTTAGCATATACCAATGATATATCTTGTGTCGAGTCGTCTGCAAAAGTAAA 867

Db 415 -----ThrGluProTrpThrGlyThrPheThrSerThrSerThrGluValThr----- 430

Qy 868 CCTTTCACCTTAAAGATGGACTGGATCAAGAATAGATGAT----- 906

Db 431 -----ThrIleThrGlyThrAsnGlyGlnProThrAspGluThrValIleValIleArg 448

Qy 907 ---GCCGGATCTAACCGTATTTGTCATTGTTGTCTACA-----ACTAGAACAGTTACA 954

Db 449 ThrProThrSerGluGlyLeuIleThrThrThrGluProTrpThrGlyThrPheThr 468

Qy 955 GACAGTACCACCTGCTGCTACTACTTCCATTCATTCCAAGTGTGTGATAAAACCAACAA 1014

Db 469 SerThrSerThrGluMetThrThrValThrGlyThrAsnGlyGlnProThrAspGluThr 488

Qy 1015 ATCGAAATTTTGCACT-----ATCCACCACT----- 1044

Db 489 ValIleValIleArgThrProThrSerGluGlyLeuIleSerThrThrGluProTrp 508

Qy 1045 -----ACCATCACAACTTCATATGTTGTGTGACTACTTCCTATCTGACTAAGACTGCA 1098

Db 509 ThrGlyThrPheThrSerThrSerThrGluValThrThrIleThrGlyThrAsnGlyGln 528

Qy 1099 CCAATTTGGTGAACAGCTACTGTTATT---GTTGATGTGCCATATCATACTACCACAACT 1155

Db 529 ProThrAspGluThrValIleValIleArgThrProThrSerGluGlyLeuIleThrThr 548

Qy 1156 GTTACCAGTGAATGGACAGAACAACTCACT-----ACCACCACAACT 1197

Db 549 ThrThrGluProTrpThrGlyThrPheThrSerThrSerThrGluMetThrThrValThr 568

Qy 1198 CGTACCACAT-----CCAACTGATTCATTAATTCACACAGTGTGTGTA 1236

Db 569 GlyThrAsnGlyGlnProThrAsp-----GluThrValIleVal 581

RESULT 14

AC2224

hypothetical protein all3346 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C:Accession: AC2224

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An.

A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AC2224
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1428 <CUR>
A;Cross-references: UNIPROT:Q8YRU7; GB:BA000019; PIDN:BAB75045.1; PID:g17132441; GSPDB:C
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all3346

Alignment Scores:
Pred. No.: 0.000221 Length: 1428
Score: 161.00 Matches: 118
Percent Similarity: 33.40% Conservative: 43
Best Local Similarity: 24.48% Mismatches: 191
Query Match: 7.01% Indels: 130
DB: 2 Gaps: 24

US-09-715-876-7_COPY_52_1296 (1-1245) x AC2224 (1-1428)

QY	34	TCATTAACCTGGTCCCAATCTGCTAAT-----TATGCTTTCARAGGCCAGGATACCCA	87
DB	808	SerValThrGluAspGlyThrProAsnLeuIleTyrThrPheThrArgThrGlySerThr	827
QY	88	ACTTGCATGCTGTTTGGGTGGTCCTTAGATGCTACAGTCCAGTCCCAATCCAGGGAT---	144
DB	828	ThrAsnAlaLeuThrValAsnTyrSerValAlaGlyThrAlaThrLeuAsnThrAspTyr	847
QY	145	-----ACATTCACATGGAATATGCCA	165
DB	848	AlaGlnThrGlyAlaAlaSerPheThrAlaThrThrGlyThrIleThrPheAlaValGly	867
QY	166	TGTGTGTTTAATATACTACTTCACAAACATCTGTTGATTTAACTGCCGATGGTGTAA	225
DB	868	AlaSerThrAlaIleLeuThrIleAsnProThrAlaAspThrThrValGluSerAsnGlu	887
QY	226	TATGCTACTGTGCAATTTTATCTGTGGAAGAAATTCACAACTTTTCTACATTAACATGT	285
DB	888	ThrValAlaLeuThrLeuAlaSerGlyThrGlyTyrThrValGlyThrThrAlaVal	907
QY	286	ACT-----GTGAACGACGCTTTGAAATCA	312
DB	908	ThrGlyThrIleThrAsnAspPheProSerIleThrLeuAlaValSerProAlaSer	927
QY	313	ATTAAAGCCATTGGTACAGTT-----	333
DB	928	ValThrGluAspGlyThrProAsnLeuIleTyrThrPheThrArgThrGlySerThrThr	947
QY	334	---ACTTTACCAATTCATTCATCAATGTTGTGGAACAGGTTCA---TCAACTGATTGGAA	387
DB	948	AsnAlaLeuThrIleAsnPheGlyValAlaGlyThrAlaThrLeuAsnThrAspTyrAla	967
QY	388	GATTCCT-----AAATGTTTACTGCTGTTACCAATACAGTCACATGTTAATGATGGTGT	441
DB	968	GlnSerGlyAlaAlaSerPheThrAlaThrThrGlyThrIleThrPheAlaAlaGlyAla	987
QY	442	AAAGATATCTCAATTGATGTTGAGTTGAAAGTCAACGGTTGATCCAAAGTCATATTG	501
DB	988	SerThrAlaIleLeu-----ThrIleAsnProThrAla	998
QY	502	TATGCTTCCAGAGTTATGCCAAGTCTCAATAAGGTCAACAATCTTTTGTGACCAACAA	561
DB	999	-----AspThrThrValGluSerAsnGluThrValAlaLeuThrLeuAla	1013
QY	562	TGTGAATAATGGTTTACACATCTGGTACAAATGGGGTCTCCAGTAGTAAAGCGTGTGCT	621
DB	1014	SerGlyThrGlyTyrThrValGlyThrThr-----ThrAlaValThrGlyThrIleThr	1031
QY	622	ATTGATGCTCAAAATATTCATATGTTATCAAAAAGGATTAAATGATTGGAATATCCG	681
DB	1032	AsnAsp---AspThrLeuProThrGlyIleThrIleAsnLeuSerGlySerGlnThrIle	1050
QY	682	GTT-----TCATCTGAATCATTTAGTTACACTAAACTTGTACATCTAATGGA	729

DB	1051	ValGluGlyAsnSerSerProGlnAsnValThrTyrThrValThrLeuSerGlnAlaSer	1070
QY	730	ATTCCAGATTAAATATCAAAATGTACCTGCTGTTATCGTCCATTTATTTGATGCTTATATT	789
DB	1071	SerGlnIle-----lleThrValGlnTyrAla	1079
QY	790	TCGTCTACAGATGTTAACCAATATATCTTTAGCATATATACCAATGATTTATCTGTGCTGGC	849
DB	1080	ThrAlaAsnGly-----ThrAlaThrAlaGlySerAspTyrThrSerThrThr	1095
QY	850	AGTCGCTCTGCAAGTAAACCT-----	870
DB	1096	GlyThrLeuThrPheAsnProGlyGluThrSerIysValIleAsnIleProIleLeuAsn	1115
QY	871	-----TTCACCTTTAAGATGGACTGGTGCATACACAAAGATAGT	903
DB	1116	AspSerValAsnGluAlaAsnGluThrPheThrLeuArgLeuThrSerProThrAsnAla	1135
QY	904	GATGCCGATCTAACGGTATTGTTCATTTGTGTACAACTAGAACAGTTTACAGAC-----	957
DB	1136	ThrLeuGlyThrThrAsnThrVal-----ThrThrThrIleThrAspThrLeu	1151
QY	958	AGTACCACTGCTGCTACTACTTTTACCATTCATTCACCAAGTGTGTGATAAAACCAATC	1017
DB	1152	SerAlaSerValThrThrThrLeuProThrAsn-----Val	1163
QY	1018	GAATTTTTCACCTATTCACCACTTCCACCATTCACATCACA---ACTTCATATGTTGGTGTGACT	1074
DB	1164	GluAsnLeuThrLeuThrGlyThrAlaIleAsnGlyThrGlyAsnAlaGly-----	1181
QY	1075	ACTTCCTATCTGACTAAGACTGCACCAATTTGGTGAACACAGCTACTGTTATTGTTGAT---	1131
DB	1182	AsnAsnIleLeuThr-----GlyAsnSerGlyAsnAsnIleLeuSerGly	1196
QY	1132	---GTGCCATATCATACTACCAACATGTTTACCAAGTGAATGGACAGGAACATCACTACC	1188
DB	1197	GlyAlaGlyAsnAspThrTyrAlaPheValAlaAlaAlaLeuGlyThrAspThrIle	1216
QY	1189	ACCACAACTCGTACCAATCCCACTGATTCAATTATTCATGAC-----ACAGTGTGTGTA	1236
DB	1217	ThrGluThrAlaThrThrGlyIleAspThrIleAspPheAsnGlySerThrAlaThrVal	1236
QY	1237	CAAGTT 1242	
DB	1237	ArgVal 1238	

RESULT 15

T22696
hypothetical protein F55B11.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22696
R;Ainscough, R.
submitted to the EMBL Data Library, December 1996
A;Reference number: Z19601
A;Accession: T22696
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-851 <WIL>
A;Cross-references: UNIPROT:Q17893; EMBL:Z83318; PIDN:CAB05903.1; GSPDB:GN00022; CESP:
A;Experimental source: clone F55B11
C;GeneticID:
A;Gene: CESP:F55B11.3
A;Map position: 4
A;Introns: 49/3; 123/3; 226/1; 282/3; 669/3; 743/3

Alignment Scores:
Pred. No.: 0.00051 Length: 851
Score: 156.00 Matches: 87
Percent Similarity: 31.40% Conservative: 32
Best Local Similarity: 22.96% Mismatches: 170
Query Match: 6.79% Indels: 90

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DB:                2                Gaps:                11
US-09-715-876-7_COPY_52_1296 (1-1245) x T22696 (1-851)
QY 124 ACCAGTCCCAATCCAGGGGATACATTCACATTCGAATGCGATGGTTAAATATACT 193
DB 330 ThrThrProSerGluLeuSerThrThrThrAlaSerValPro----- 343
QY 184 ACTTCACAAACATCTGTTGATTTAACTGCCGATGGTGTAAATATGCTACTTGTCAATTT 243
DB 344 ThrThrThrThrSerValProThrThrThrThrThrValProThrThrThr----- 360
QY 244 TATTCGTGTGAAGAATTACAACTTTTTCACATTAACATGTACTGTGAACGCGTTTG 303
DB 361 -----ThrThrValProThrThrThrThrThrThrThrThrThrThr----- 373
QY 304 AATCATCCATTAAAGCATTTGGTACAGTTACTTTACCAATTCATTCATTTGGTGA 363
DB 374 -----ThrThrValPro----- 378
QY 364 ACAGGTTTCATCAACTGATTTGGAAGATTTCTAAATGTTTACTGCTGGTACCAATACAGTC 423
DB 379 -----ThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 396
QY 424 ACATTTAATGATGGTGATAAGATATCTCAATTGATGTTGAGTTTGAAGAGTCAACCGTT 483
DB 397 Thr-----ValProThrThrThrThrVal----- 405
QY 484 GATCCAAGTGCAATATTTGTATGTCTCCAGAGTTATGCCAAGTCTCAATAAGGTCACAACT 543
DB 406 Pro-----ThrThr----- 408
QY 544 CTTTTTGGGCCACCACCAATGGAATGGTTTACACATCTGTCACAAATGGGGTCTCCAGT 603
DB 409 ThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 428
QY 604 AGTAACGGTGACGTTGATTTGATGCTCAAAATATCATATTTGGTATCACAAGGATTA 663
DB 429 ThrThrThrThrThrThrThrThrThrThrThrThrVal----- 440
QY 664 AATGATGGAATATTCGGTTTTCATCTGAATCATTTAGTTACATAAACT----- 714
DB 441 -----ProThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 455
QY 715 TGTCATCTAATGGAATTCAGATTAATAATATCAAAATGTACCTGCTGGTTATCGTCCATTT 774
DB 456 ThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 470
QY 775 ATTGATGCTTATATTTCTGCTACAGATGTTAAACCAATATATCTTTAGCATATACCAATGAT 834
DB 471 -----ThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 485
QY 835 TATACTTGTGTCGAGTCGTCGCAAGTAAGACCTTTTCACTTTAAGATGGACTGGATAC 894
DB 486 ThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 505
QY 895 AAGAAATAGTATGCCGATCTAAACGGTATTTGTCATCTGTTGTGTACAACTAGAAACAGTTACA 954
DB 506 ThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 525
QY 955 GACAGTACCACTGCTGCTACTTTCACCACTACCATTCACAACTTGTGTGATGAGTGTGACT 1014
DB 526 ThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 545
QY 1015 ATCGAAATTTGCAACCTATTTCCACCACTACCATTCACAACTTGTGTGATGAGTGTGACT 1074
DB 546 ProThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 565
QY 1075 ACTTCCTATCTGACTAGACCTGCACCAATTTGGTGAACAGCT-----ACTGTTATTGTT 1128
DB 566 ValProThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 585
QY 1129 GATGTGCCATATCATATACCACTGTTTACCAGTGAATGGACAGGAACAACTCACTACC 1188
```

```
DB 586 ThrValPro-----ThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 604
QY 1189 ACCACAACCTCGTACCAATCCAACTGATTCAAATTTGACACAGTGGTGGTACAAAGTTCCA 1245
DB 605 ThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 623

Search completed: September 8, 2005, 17:51:13
Job time : 81 secs
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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 8, 2005, 17:10:51; Search time 200 Seconds

(without alignments)
4815.167 Million cell updates/sec

Title: US-09-715-876-7_COPY_52_1296

Perfect score: 2297

Sequence: 1 aagacaatcactggtgtttt.....cagtggtgggtcaagtcca 1245

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgm2_1/USPTO_spool_p/US097115876/runat_08092005_172226_18474/app_query.fasta_1.1415
-DB=A_Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US097115876 @CGN_1_1_224 @runat_08092005_172226_18474 -NCPUS=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_16Dec04:*
1: Geneseq1980a:*
2: Geneseq1990a:*
3: Geneseq2000a:*
4: Geneseq2001a:*
5: Geneseq2002a:*
6: Geneseq2003a:*
7: Geneseq2003bs:*
8: Geneseq2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2174	94.6	1260	7 ABW01168	Abw01168 Candida a
2	1885	82.1	1119	7 ABW01170	Abw01170 Candida a
3	1865	81.2	1270	7 ABW01172	Abw01172 Candida a
4	1832	79.8	1047	7 ABW01175	Abw01175 Candida a
5	1769.5	77.0	468	7 ABW01169	Abw01169 Candida a
6	1596	69.5	469	7 ABW01171	Abw01171 Candida a
7	1544.5	67.2	468	7 ABW01176	Abw01176 Candida a
8	1500	65.3	1443	7 ABW01173	Abw01173 Candida a
9	961.5	41.9	2297	7 ABW01174	Abw01174 Candida a
10	308.5	13.4	650	2 AAR47575	Aar47575 Alpha-agg

11	308.5	13.4	650	8 ADS43747	Ads43747 Bacterial
12	179	7.8	800	8 ABO58564	AbO58564 Human gen
13	179	7.8	1296	5 ABG66756	Abg66756 Human nov
14	179	7.8	1296	5 ABG66702	Abg66702 Human nov
15	177	7.7	1322	8 ADN18700	Adn18700 Bacterial
16	177	7.7	1537	2 AAR60562	Aar60562 Yeast 4.7
17	177	7.7	1537	8 ADP87475	Adp87475 S cerevis
18	177	7.7	1537	8 ADN18745	Adn18745 Bacterial
19	175.5	7.6	1837	3 AAB11726	Abj11726 Cryptospo
20	175.5	7.6	1837	5 ABJ04044	Abj04044 C parvum
21	175	7.6	1721	3 AAW48299	Aaw48299 Cryptospo
22	175	7.6	1721	3 AAB11727	Abj11727 Portion o
23	175	7.6	1721	5 ABJ04045	Abj04045 C parvum
24	172	7.5	1217	8 ADQ29696	Adq29696 Human col
25	170	7.4	957	7 ADD47260	Add47260 Human pro
26	170	7.4	957	7 ADE58049	Ade58049 Human pro
27	170	7.4	957	7 ADD47264	Add47264 Human pro
28	170	7.4	957	7 ADE58045	Ade58045 Human pro
29	163	7.1	738	7 ADC01840	Adc01840 C. albica
30	161.5	7.0	1075	8 ADS43638	Ads43638 Bacterial
31	156	6.8	688	4 AAM16315	Aam16315 Peptide #
32	156	6.8	688	4 ABB35307	Abb35307 Peptide #
33	156	6.8	688	4 AAM28810	Aam28810 Peptide #
34	156	6.8	688	4 ABB30137	Abb30137 Peptide #
35	156	6.8	688	4 ABB20749	Abb20749 Protein #
36	156	6.8	688	4 AAM68511	Aam68511 Human bon
37	156	6.8	688	4 AAM56138	Aam56138 Human bra
38	156	6.8	688	4 AAG50180	Abg50180 Human liv
39	156	6.8	688	4 AAM04053	Aam04053 Peptide #
40	156	6.8	688	5 ABG38092	Abg38092 Human pep
41	155	6.7	894	2 AAR58754	Aar58754 S. cerevi
42	155	6.7	894	2 AAR47578	Aar47578 Flocculat
43	155	6.7	1180	5 ABB54070	Abb54070 Lactococc
44	154	6.7	1283	8 ADS44186	Ads44186 Bacterial
45	153.5	6.7	1795	4 ABB69806	Abb69806 Drosophil

ALIGNMENTS

RESULT 1

ABW01168
ID ABW01168 standard; protein; 1260 AA.

XX AC ABW01168;

XX DT 15-JAN-2004 (first entry)

XX DE Candida albicans agglutinin-like sequence (ALS) 1 protein.

XX KW Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;

XX KW candidiasis; vaccine; fungicide.

XX OS Candida albicans.

XX PN US2003124134-A1.

XX PD 03-JUL-2003.

XX PF 13-SEP-2002; 2002US-00245802.

XX PR 19-NOV-1999; 99US-0166663P.

XX PR 18-NOV-2000; 2000US-00715876.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Edwards JE, Filler SG, Sheppard DC, Ibrahim A, Fu Y;

XX WPI; 2003-810971/76.

XX DR N-P8DB; AD62305.

XX New monoclonal antibody against Candida albicans agglutinin-like sequence
PT 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
PT candidiasis, or to generate an immune response that blocks adherence of

PT the organism.

XX Disclosure; Page 14-17; 65pp; English.

XX The present invention relates to a monoclonal antibody against an agglutinin-like sequence (ALS)1 protein that specifically binds an epitope in an N-terminal domain and which inhibits adherence of Candida albicans to endothelial cells. The invention is useful as vaccines for treating and preventing disseminated candidiasis and for generating an immune response capable of blocking adherence of the organism. The invention is also useful in gene therapy. The present sequence is Candida albicans agglutinin-like sequence (ALS) protein

XX Sequence 1260 AA;

Alignment Scores:

Pred. No.: 6,1e-199 Length: 1260
Score: 2174.00 Matches: 413
Percent Similarity: 99.52% Conservative: 2
Best Local Similarity: 99.52% Mismatches: 0
Query Match: 94.65% Indels: 0
DB: 7 Gaps: 0

US-09-715-876-7_COPY_52_1296 (1-1245) x ABW01168 (1-1260)

QY 1 AAGCAATCACTGGTGTGTTTGTAGTATTAATTCATTAACTTGGTCCAATGCTGCTAAT 60
DB 18 LysThrIleThrGlyValPheAspSerPheAsnSerLeuThrTrpSerAsnAlaAsn 37
QY 61 TATGCTTTCAAGGCCAGGATCCCAACTTGGAAATCTGTTTGGGTTCCTTAGAT 120
DB 38 TyrAlaPheLysGlyProGlyTyrProThrTrpAsnAlaValLeuGlyTrpSerLeuAsp 57
QY 121 GGTACAGTGCATTCAGGGGATACATTACATTGAATATGCCATGCTGTTTAATAT 180
DB 58 GlyThrSerAlaAsnProGlyAspThrPheThrLeuAsnMetProCysValPheLysTyr 77
QY 181 ACTACTTCAACAACATCTGTTGATTAACTGCCGATGGTGTAAATATGCTACTTGTCAA 240
DB 78 ThrThrSerGlnThrSerValAspLeuThrAlaAspGlyValLysTyrAlaThrCysGln 97
QY 241 TTTTATTCTGGTGAAGAATTACAACTTTTCTACATTAACATGACTGTGAAGCAGCT 300
DB 98 PheTyrSerGlyGluGluPheThrThrPheSerThrLeuThrCysThrValAsnAspAla 117
QY 301 TTGAATCATCATTAAGCATTTGGTACAGTACTTTTACCAATTCATTCATTCATTTGGT 360
DB 118 LeuLysSerSerIleLysAlaPheGlyThrValThrLeuProIleAlaPheAsnValGly 137
QY 361 GGAACAGGTTTCATCAACTGATTTCGAAGATTCTAAATGTTTACTGCTGGTACCAATACA 420
DB 138 GlyThrGlySerSerThrAspLeuGluAspSerLysCysPheThrAlaGlyThrAsnThr 157
QY 421 GTCATATTAAATGATGATAAGATATCTCAATTCATTCATTCATTCATTCATTCATTCATTC 480
DB 158 ValThrPheAsnAspGlyAspLysAspIleSerIleAspValGluPheGluLysSerThr 177
QY 481 GTTCATCCAGTGCATATTTGTATGCTTCCAGATGTTATGCCAGTCTCAATTAAGTCCACA 540
DB 178 ValAspProSerAlaTyrLeuTyrAlaSerArgValMetProSerLeuAsnLysValThr 197
QY 541 ACTCTTTTGTGGCACCACATGTCGAAATGGTTACATCTGGTACATCTGGTACATGGGGTCTCC 600
DB 198 ThrLeuPheValAlaProGlnCysGluAsnGlyTyrThrSerGlyThrMetGlyPheSer 217
QY 601 AGTAGTAACGGTGCATTTGCTATTGATTGCTCAATATTCATATTCATATTCATATTCATATTC 660
DB 218 SerSerAsnGlyAspValAlaIleAspCysSerAsnIleHisIleGlyIleThrLysGly 237
QY 661 TTAATATGTAATTCGGTTCATCTCAATCATTTAGTACACTTAAACTTGTGATCA 720
DB 238 LeuAsnAspTrpAsnTyrProValSerSerGluSerPheSerTyrThrLysThrCysThr 257

QY 721 TCTAATGGAATTCAGATTAAATATCAAAATGATGACCTGCTGGTTATCGTCCATTATTATGAT 780
DB 258 SerAsnGlyIleGlnIleLysTyrGlnAsnValProAlaGlyTyrArgProPheIleAsp 277
QY 781 GCTTATATTCTGCTACAGATCTTAACCAATATCTTTAGCATATATACCAATGATTATCT 840
DB 278 AlaTyrIleSerAlaThrAspValAsnGlnTyrThrLeuAlaTyrThrAsnAspTyrThr 297
QY 841 TGTGCTGGCAGTCTGCTGCAAGATAAACCTTTTCACTTTAAGATGGAAGTACCAAGAT 900
DB 298 CysAlaGlySerArgSerGlnSerLysProPheThrLeuArgTyrThrGlyTyrLysAsn 317
QY 901 AGTGATGCCGATCTTAACGGTATGTTCATTTGTTGTCTACCACTAGAACAGTTACAGACGT 960
DB 318 SerAspAlaGlySerAsnGlyIleValIleValAlaThrThrArgThrValThrAspSer 337
QY 961 ACCACTGCTGCTCACTACTTTTACCATTCATCCAAAGTGTGTGATAAACAACAATCGAA 1020
DB 338 ThrThrAlaValThrThrLeuProPheAsnProSerValAspLysThrLysThrIleGlu 357
QY 1021 ATTTTCAACCTATTCCAACTACCACTACCACTACCACTTTCATATGTTGGTGTGACTTCC 1080
DB 358 IleLeuGlnProIleProThrThrThrIleThrThrSerTyrValGlyValThrThrSer 377
QY 1081 TATCTGACTAAGACTGCACTCAATTTGGTGAAACAGCTACTGTTTATTTGATGTCATAT 1140
DB 378 TyrSerThrLysThrAlaProIleGlyGluThrAlaThrValIleValAspValProTyr 397
QY 1141 CATACTACCACTGTTTACCACTGATGAGCAGGAGCAACATCACTACCACTCACTCGT 1200
DB 398 HisThrThrThrThrValThrSerGluTrpThrGlyThrIleThrThrThrThrThrArg 417
QY 1201 ACCAATCCAACTGATTCAATTTGACACAGTGGTGTGACAAAGTTCCA 1245
DB 418 ThrAsnProThrAspSerIleAspThrValValValGlnValPro 432
RESULT 2
ABW01170
ID ABW01170 standard; protein; 1119 AA.
XX
XX ABW01170;
AC
XX
XX 15-JAN-2004 (first entry)
DT
XX
XX
DE Candida albicans agglutinin-like sequence (ALS) 3 protein.
XX
XX Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;
XX candidiasis; vaccine; fungicide.
XX
XX Candida albicans.
XX
XX US2003124134-A1.
XX
XX 03-JUL-2003.
PD
XX
XX 13-SEP-2002; 2002US-00245802.
PF
XX
XX 19-NOV-1999; 99US-0166663P.
PR
XX
XX 18-NOV-2000; 2000US-00715876.
XX
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
PA
XX
XX Edwards JE, Fuller SG, Sheppard DC, Ibrahim A, Fu Y;
PI
XX
XX WPI; 2003-810971/76.
DR
XX
XX N-PSDB; AAD62307.
DR
XX
XX New monoclonal antibody against Candida albicans agglutinin-like sequence
PT 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
PT candidiasis, or to generate an immune response that blocks adherence of
PT the organism.
XX
XX Disclosure; Page 21-23; 65pp; English.
PS

XX The present invention relates to a monoclonal antibody against an
CC agglutinin-like sequence (ALS)1 protein that specifically binds an
CC epitope in an N-terminal domain and which inhibits adherence of Candida
CC albicans to endothelial cells. The invention is useful as vaccines for
CC treating and preventing disseminated candidiasis and for generating an
CC immune response capable of blocking adherence of the organism. The
CC invention is also useful in gene therapy. The present sequence is Candida
CC albicans agglutinin-like sequence (ALS) protein
XX
XX Sequence 1119 AA;
SQ

Qy	781	GCTTATATTCTGCTACAGATGTTAACCAATATATCTTACCATATACCAATGATTACT	840
Db	278	AlaTyriLeSerAlaThrAspValaAsnSerTyThrLeuSerTyZrAlaAsnGluTyThr	297
Qy	841	TGTGCTGGCAGTCGTCTGCAAACTAAACCTTTTACACTTTTAAGATGGAGCTGGATACAAGAAT	900
Db	298	CysAlaGlyGlyTyTrpGlnaGalaProPheThrLeuArgTrpThrGlyTyZrAspAsn	317
Qy	901	AGTGATGCCGGATCTTAACCGGTATTGTTCATTTGTGTCTCAACTAGACAGCTTACAGACAGT	960
Db	318	SerAspAlaGlySerAsnGlyIleValIleValAlaThrThrArgThrValThrAspSer	337
Qy	961	ACCACCTGCTCTACTCTTTTACCATTCAATCCCAAGTGTTCATAAAACCAAAACAATCGAA	1020
Db	338	ThrThrAlaValThrThrLeuProPheAspProAsnArgAspIysThrIysThrIleGlu	357
Qy	1021	ATTTTGCAACCTATTCCAACCTACCATCACAACCTTCATATGTTGGTGGACTACTCTCC	1080
Db	358	IleLeuIysProIleProThrThrThrIleThrThrSerTyZrValGlyValThrThrSer	377
Qy	1081	TATCTGACTAAGACTGCACCAATTTGTGGAAACAGCTACTGTTATTTGTTGATGGCCATAT	1140
Db	378	TyrSerThrIysThrAlaProIleGlyGluThrAlaThrValIleValAspIleProTyZr	397
Qy	1141	CATACTACCACAACCTGTTTACAGTGAATGACAGGAACAATCACTACCAACCAACCTCGT	1200
Db	398	HisThrThrThrThrValThrSerIysTrpThrGlyThrIleThrSerThrThrThrHis	417
Qy	1201	ACCAATCCAACCTGATTCATCAATTTGACACAGTGGTGGTACAAGTTCCA	1245
Db	418	ThrAsnProThrAspSerIleAspThrValIleValGlnValPro	432

RESULT 3

ABW01172
ID ABW01172 standard: protein: 1270 AA.

XX
AC ABW01172:

15-JAN-2004 (first entry)

XX DE *Candida albicans* agglutinin-like sequence (ALS) 5 protein.

xx Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;
kw candidiasis; vaccine; fungicide.

XX
OS
Candida albicans.XX
PN US2003124134-A1.XX
PD 03-JUL-2003.

13-SEP-2002: 2002US-00245802.

XX
PR 19-NOV-1999: 99US-0166663P.

PR 18-NOV-2000; 2000US-00715876.
YY

PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

PI Edwards JE, Filler SG, Sheppard DC, Ibrahim A, Fu Y, vv

DR WPI; 2003-810971/76.

XX New monoclonal antibody against *Candida albicans* agglutinin-like sequence
PT
PT 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
PT candidiasis, or to generate an immune response that blocks adherence of
PT the organism.

XX
PS Disclosure: Page 27-31: 65pp; English.

XX
CC
CC
CC
CC
CC

CC immune response capable of blocking adherence of the organism. The
 CC invention is also useful in gene therapy. The present sequence is Candida
 CC albicans agglutinin-like sequence (ALS) protein
 XX
 SQ Sequence 1047 AA;

Alignment Scores:
 Pred. No.: 3,49e-166 Length: 1047
 Score: 1832.00 Matches: 346
 Percent Similarity: 92.05% Conservativeness: 36
 Best Local Similarity: 83.37% Mismatches: 33
 Query Match: 79.76% Indels: 0
 DB: 7 Gaps: 0

US-09-715-876-7_COPY_52_1296 (1-1245) x ABW01175 (1-1047)

Qy 1 AAGCAATCACTGCTGTTTGTAGTATTAAATTCATTAACTTGGTCCAAATGCTGCTAAT 60
 Db 18 LysThrIleThrGlyValPheAsnSerPheAsnSerLeuThrThrSerAsnAlaAlaThr 37
 Qy 61 TATGCTTTCAAGGCCAGGATCCCAACTTGGATGCTGTTTGGTGGTCTCTAGAT 120
 Db 38 TyrHisTyrLysGlyProGlyThrProThrTyrAsnAlaValLeuGlyTyrSerLeuAsp 57
 Qy 121 GGTACCAAGTGCATCCAGGGATACATTCATTTGAATATGCCATGTGTTTAAATAT 180
 Db 58 GlyThrSerAlaSerProGlyAspThrPheThrLeuAsnMetProCysValPheLysPhe 77
 Qy 181 ACTACTTCACAAACATCTGTTGATTTAACTCCGATGGTGTAAATATGCTACTTGTCAA 240
 Db 78 ThrThrSerGlnThrSerValAspLeuThrAlaHisGlyValLysTyrAlaThrCysGln 97
 Qy 241 TTTTATCTGCTGAGAGATTCACAACTTTCTACATTAACATCTACTGTGAAGCAGCT 300
 Db 98 PheGlnAlaGlyGluGluPheMetThrPheSerThrLeuThrCysThrValSerAsnThr 117
 Qy 301 TTGAAATCATCATTAAGCATTTGGTACAGTACTTTTACCAATTCATCAATGCTGTTGGT 360
 Db 118 LeuThrProSerIleLysAlaLeuGlyThrValThrLeuProLeuAlaPheAsnValGly 137
 Qy 361 GGAACAGGTTTCATCACTGATTTGAAGATTTCTAAATGTTTACTGCTGGTACCAATACA 420
 Db 138 GlyThrGlySerSerValAspLeuGluAspSerLysCysPheThrAlaGlyThrAsnThr 157
 Qy 421 GTCACATTTATGATGGTGAATAAGATATCTCAATTTGATGTTGATTTGAAGTCAACC 480
 Db 158 ValThrPheAsnAspGlyGlyLysLysIleSerIleAsnValAspPheGluArgSerAsn 177
 Qy 481 GTTGATCCAAGTGCATATTTGTATGCTTCCAGAGTTATGCCAAGTCTCAATAAGTCACA 540
 Db 178 ValAspProLysGlyTyrLeuThrAspSerArgValIleProSerLeuAsnLysValSer 197
 Qy 541 ACTCTTTTGTGGCCACCAATGTGAAATGTTTACACATCTGGTACCAATGGGTCTCC 600
 Db 198 ThrLeuPheValAlaProGlnCysAlaAsnGlyTyrThrSerGlyThrMetGlyPheAla 217
 Qy 601 AGTAGTAACGCTGAGTGTCTATTCATTCCTCAATATTCATATTCATTCATCAAAAGGA 660
 Db 218 AsnThrTyrGlyAspValGlnIleAspCysSerAsnIleHisValGlyIleThrLysGly 237
 Qy 661 TTAATGATTTGAATATTCGCTTTTCATCTGAATCATTTAGTTAGTACACTAAATCTGTACA 720
 Db 238 LeuAsnAspTyrAsnTyrProValSerSerGluSerPheSerTyrThrLysThrCysSer 257
 Qy 721 TCTAATGGAATTCAGATTAATATCAAAATGTACTGCTGCTGTTATCGTCCATTTATGAT 780
 Db 258 SerAsnGlyIlePheIleThrTyrLysAsnValProAlaGlyTyrArgProPheValAsp 277
 Qy 781 GCTTATATTCGCTACAGATGTTAAACCAATATATCTTTAGCATATACCAATGATTATACT 840
 Db 278 AlatyIleSerAlaThrAspValAsnSerTyrThrLeuSerTyrAlaAsnGluTyrThr 297
 Qy 841 TGTGCTGCGAGTCTGCTCAAGATTAACCTTTCACTTCTAAGATGCTGGTCAAGAAT 900

Db 298 CysAlaGlyGlyTyrTyrGlnArgAlaProPheThrLeuArgTyrThrGlyTyrArgAsn 317
 Qy 901 AGTGATGCGGATCTAAACGGTATTGTTCATTGTGTACCAACTAGAACAGTTACAGACAGT 960
 Db 318 SerAspAlaGlySerAsnGlyIleValIleValAlaThrThrArgThrValThrAspSer 337
 Qy 961 ACCACTGCTGTCTACTACTTTTACCAATTCATCCAAAGTGTGTGATAAACCAAAACAATCGAA 1020
 Db 338 ThrThrAlaValThrThrLeuProPheAspProAsnArgAspLysThrLysThrIleGlu 357
 Qy 1021 ATTTGCAACCTATTCCAACCACTACCATCACAACCTTCATATGTTGGTGTGACTACTTCC 1080
 Db 358 IleLeuLysProIleProThrThrIleThrThrSerTyrValGlyValThrThrSer 377
 Qy 1081 TATCTGCTGAAGACTGCACCAATTTGGTGAACAGCTACTCTTATTTGTGTGATGTCATAT 1140
 Db 378 TyrSerThrLysThrAlaProIleGlyGluThrAlaThrValIleValAspIleProTyr 397
 Qy 1141 CATACTACCACTGTTTACCACTGAATGACAGGAACTCACTACCACTACCACTCACTCGT 1200
 Db 398 HisThrThrThrThrValThrSerLysTyrThrGlyThrIleThrSerThrThrThrHis 417
 Qy 1201 ACCAATCCAACTGATTCATTTGACACAGCTGCTGTGCTACCAAGTTCCA 1245
 Db 418 ThrAsnProThrAspSerIleAspThrValIleValGlnValPro 432

RESULT 5

ABW01169
 ID ABW01169 standard; protein; 468 AA.

AC ABW01169;

DT 15-JAN-2004 (first entry)

XX Candida albicans agglutinin-like sequence (ALS) 2 protein.

XX Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;
 XX candidiasis; vaccine; fungicide.

XX Candida albicans.

XX Key Location/Qualifiers

FT Misc-difference 41 /note= "Encoded by AAC"

XX US2003124134-A1.

XX 03-JUL-2003.

XX 13-SEP-2002; 2002US-00245802.

XX 19-NOV-1999; 99US-0166663P.

XX 18-NOV-2000; 2000US-00715876.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Edwards JB, Filler SG, Sheppard DC, Ibrahim A, Fu Y;

XX WPI; 2003-810971/76.

XX N-PSDB; AAD62306.

XX New monoclonal antibody against Candida albicans agglutinin-like sequence
 CC 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
 CC candidiasis, or to generate an immune response that blocks adherence of
 CC the organism.

XX Disclosure; Page 18-19; 65pp; English.

XX The present invention relates to a monoclonal antibody against an
 CC agglutinin-like sequence (ALS)1 protein that specifically binds an
 CC epitope in an N-terminal domain and which inhibits adherence of Candida
 CC albicans to endothelial cells. The invention is useful as vaccines for

CC treating and preventing disseminated candidiasis and for generating an
CC immune response capable of blocking adherence of the organism. The
CC invention is also useful in gene therapy. The present sequence is Candida
CC albicans agglutinin-like sequence (ALS) protein

Sequence 468 AA;

Alignment Scores:		
Pred. No.:	2,378-160	468
Score:	1769.50	333
Percent Similarity:	86.75%	27
Best Local Similarity:	80.24%	Conservative: 54
Query Match:	77.04%	Mismatches: 1
DB:	7	Indels: 1
		Gaps: 1

US-09-715-876-7 COPY 52 1296 (1-1245) x ABW01169 (1-468)

QY 1 AAGACAATCACTGGTGTGTTTTTATGATAGTTTAAATTCATTAACTGGTCCAAATGCTGCTAAT 60

Dh 18 IvtelvaIYethrgIvWaItheanSerPheanSerLeuThrThrAraaAGIvAsn 37

61 TATGTTTCAAAGGCCAGGATACCCAACTTGGATGCTGTTTGGTGGTCTTAGAT 120

Db 38 TyrAlaTyrLysGlyProAsnArgProThrIrpAsnAlaValLeuGlyTyrSerLeuAsp 57

QY 121 GGTACCAAGTGCCTAATCCAGGCGGATAATTCATTCATTAATGATATGCATGATGATTTAAATAT 181

Db 58 GlyThrSerAlaasnProGlyAspThrPheThrLeuasnMetProCysValPhelysPhe 77

QY 181 ACTACTTCACAAACATCTGTTGATTAACTGCCGATGGTGTAAATATGCTACTTGTCAA 240

Db 78 IleThrAspGlnThrSerValAspLeuThrAlaGluGlyValIstyrAlaThrCysGln 97

Qy	241	TTTATAATCTGGTGAAGAAATTCACAACTTTTCTATCATTAACATGTACTCTGAAACGACGCT	117
Db	98	PhetvSergLvGlulvPhetvThrPheserSergLeulvSvsthrValSeraasThr	117

QY	301	TTGAAATCATCCATTAAAGGCATTGGTACAGTTACTTTACCAATTGCATTCAATGTTGGT	360
QY	301	TTGAAATCATCCATTAAAGGCATTGGTACAGTTACTTTACCAATTGCATTCAATGTTGGT	360

Db 118 LeuThrSerSerIleLysAlaLeuGlyThrValThrLeuProIleSerPheAsnValGly 137

	GGAA	CAGGTT	CATCA	CTGATT	TGGGA	GATTC	TAAAT	GTCTTTT	ACTGCT	TGTACCA	AATA	CA	422
QY	361												
								:	:	:	:		
pB	138	GLVThr	GLVSer	SerVal	LapLeu	GLUser	SerGln	Cysapp	PheLys	Ala	GLIVThr	AsnThr	157

421 GTCCACATTTAATGATGGTGATAAAGATATCTCAATTGATGTTTGAAAAAGTCAACC 480

Db 158 ValThrPheAsnAspGlyAspLysLysIleSerIleAspValAspPheGluLysThrAsn 177

QY	481	GTTGATCCCAAGTGCATATTGTGATGCTTCCAGAGTATTGCCCAAGTCTCTCAATAAGGTCA	540
Dh	178	GLUASALLASERGLVTVRPhelleAlaLaserAraLeulleProSerIleAsLvsValSer	197

25 *Cratogeomys merriami* 5'-TGGGACCAACCAATGTGAAATGGTTACACATCTGTTACAATGGGGTTCTCC 600

270 *Cratogeomys merriami* 5'-TGGGACCAACCAATGTGAAATGGTTACACATCTGTTACAATGGGGTTCTCC 600

QY 541 ACTCTTTTGTGGACCAACCAATGTGAAATGGTTACACATCTGTTACAATGGGGTTCTCC 600

Db 198 IleThrTrpValAlaProGlnCysAlaAsnGlyTyrThrSerGlyAlaMetGlyPheIle 217
:::

QY	601	AGTAGTAA	CGGTGAC	TTCATTTGGTATCACA	AAAAGA	660
NH	218	VALLI	CAU	THCCV	LENT	277

DD	216	vardeumimtyngpimimirensfcysocraasnaummsvaxayfaccumafpoc-f
QY	661	TTAAATGATTGGAAATTATCCGGTTTCATCTCGAATCATTTAGTTACACTAAAACTTGTACA

Db 238 LeuAsnAspTrpAsnPheProValSerSerAspSerLeuSerIleAsnLysThrCysSer 257

QY 721 TCTAATGGAAATTCAGATTAAATATCAAAAATGTACCTGCTGGTTATCGTCCATTATTGAT 780

DB	258	serfnrGlylleserllelnrlytGluabuvafzomaaglyyAylalGfOfuenerasp	271
QY	781	GCTTATATTCTGTCACAGTGTAAcCAATATACTTTAGCATATACCAGTATTATACT	840

Db 278 valTyrThrSerValSerGlyGlnAsnArg---GlnLeuArgTyrThrAsnAspTyrAla 296

Qy	841	TGTCCTGGCAGT	CGTCTGC	CAAGCTTAACCTTTT	CACCTTTAAGATGGG	ACTGCATACAAGAAT	900
Db	297	CysValGlySerSerLeuGlnSerIysProPheAsnLeuArgGlyIyrAsnAsn					316
Qy	901	AGTGATGCCGGATCTAACGGTATTGTTCATTTGCTGTACAACTAGAACAGTTACAGACAGT					960
Db	317	SerGluAlaAsnSerAsnGlyPheValIleValAlaIaThrThrArgThrValThrAspSer					336
Qy	961	ACCACCTGCTGCTCACTACTTTTACCATTCAATCCAAAGTGTTCATAAAACCAAAACAATCGAA					1020
Db	337	ThrThrAlaValThrThrLeuProPheAsnProSerValaspIysThrIysThrIleGlu					356
Qy	1021	ATTTTGAACCTATTCCAACCACTACCATCAACAACCTCATATGTTGGTGTGACTACTTCC					1080
Db	357	IleLeuGlnProIleProThrThrThrIleThrThrSerTyrValGlyValThrThrThrSer					376
Qy	1081	TATCTGACTAAGACTGCACCAATTTGGTGAACAGCTACTGTTATTGTTGATGTGCCATAT					1140
Db	377	TyrSerThrIysThrAlaProIleGlyGluThrAlaThrValIleValaspValProTyr					396
Qy	1141	CATACTACCACAACTGTTTACCAGTGAATGGAAGGAAACATCACTACCACCAACTCGT					1200
Db	397	HisThrThrThrThrValThrSerGluTyrThrGlyThrIleThrThrThrThrThrArg					416
Qy	1201	ACCAATCCAACTGATTCAATTTGACACAGTGGTGGTACAGTTCCA					1245
Db	417	ThrAsnProThrAspSerIleAspThrValValValGlnValPro					431

RESULT 6

ABW01171
ID ABW01171 standard; protein; 469 AA.
XX
XX AC ABW01171;
XX
XX
XX 15-JAN-2004 (first entry)
DT
DT
DE *Candida albicans* agglutinin-like sequence (ALS) 4 protein.

XX Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;
KW candidiasis; vaccine; fungicide.

XX
OS Candida albicans.

XX PN US2003124134-A1.

XX
03. III - 2003
00[illegible]

PF 13-SEP-2002; 2002US-00245802.
XX

PR 19-NOV-1999; 99US-0166663P.
PR 18-NOV-2000; 2000US-00715876.

XX
PA (HAPP-) HAPPOR-ICTA RES & EDUCATION INST.
XX[illegible]

FI EDWARDS JR, FILLER SG, SHEPPARD DC, TOLANIN S, TULLY R, XX

DR WPI; 2003-810971/76.
DR N-PSDB; AAD62308.

XX New monoclonal antibody against *Candida albicans* agglutinin-like sequence
PT
PT 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
PT candidiasis, or to generate an immune response that blocks adherence of
PT the organism.

XX PS Disclosure; Page 24-25; 65pp; English.

xx CC The present invention relates to a monoclonal antibody against an
CC agglutinin-like sequence (ALS) protein that specifically binds an
CC epitope in an N-terminal domain and which inhibits adherence of Candida
CC albicans to endothelial cells. The invention is useful as vaccines for
CC treating and preventing disseminated candidiasis and for generating an
CC immune response capable of blocking adherence of the organism. The
CC invention is also useful in gene therapy. The present sequence is Candida
CC

CC albicans agglutinin-like sequence (ALS) protein
XX
SQ Sequence 469 AA;

Alignment Scores:	1.03e-143	Length:	469
Pred. No.:	1596.00	Matches:	295
Score:	81.20%	Conservative:	42
Percent Similarity:	71.08%	Mismatches:	78
Best Local Similarity:	79.48%	Indels:	0
Query Match:	7	Gaps:	0
DB:			

US-09-715-876-7 COPY 52 1296 (1-1245) X ABW01171 (1-469)

Qy	1	AAGCAATCACTGGTGGTTTTTGATAGTTTAAATTCATTAACTTGGTCCCATGCTGCTAAT	60
Db	18	LySValIleThrGlyValPheAenSerPheAenSerLeuThrTrpAlaAenAlaAalaser	37
Qy	61	TATGCTTTCAAAGGCCAGGATACCAACTGGGAATGCTGTTTGGTTCCTTAGAT	120
Db	38	TyrProTyrArgGlyProAlaThrProThrTrpThrAlaValIleGlyTrpSerLeuAasp	57
Qy	121	GGTACCAGTCGCAATCCAGGGGATACATTCAATTCGAATATGCCATGTGTGTTAAATAT	180
Db	58	GlyAlaThrAlaSerAlaGlyAaspThrPheThrLeuAaspMetProCysValPheIysPhe	77
Qy	181	ACTACTTCACAAACATCTGTTGAATTAACCTGCCGATGGGTAAATATGCTACTTGTCAA	240
Db	78	IleThrAaspGlnThrSerIleAaspLeuValAlaAaspGlyArgThrTyrAlaThrCysAen	97
Qy	241	TTTTATCTCGTGAAGAATTCACACTTTTCTACATTAACATGTACTGTGAACGAGCT	300
Db	98	LeuAenSerAlaGluGluPheThrThrPheSerSerValSerCysThrValThrThrThr	117
Qy	301	TTGAAATCATCCATTAAAGCATTTCGTACAGTTACTTTACCAATTCATCAATGTTGT	360
Db	118	MetThrAlaAaspThrLysAlaIleGlyThrValThrLeuProPheSerPheSerValGly	137
Qy	361	GGACAGGTTTCATCAACTGATTGGAAGATTCTAAATGTTTACTGCTGGTACCATAACA	420
Db	138	GlySerGlySerAaspValAaspLeuAlaenSerGlnCysPheThrAlaGlyIleAenThr	157
Qy	421	GTCACATTAAATGATGGTGATAAAGATATCTCAATGTAGTTGAGTTTGAAAAGTCAACC	480
Db	158	ValThrPheAenAaspGlyAaspThrSerIleSerThrThrValAaspPheGlyIysSerThr	177
Qy	481	GTTGATCCAGTGCATATTTGATGCTCCAGATTATGCCAAGTCTCAATTAAGGTCACA	540
Db	178	ValAlaSerSerAaspArgIleLeuLeuSerArgIleLeuProSerLeuSerGlnAlaVal	197
Qy	541	ACTCTTTTGTGGCACCACAATGTGAAATGGTTACACATCTGGTACAATGGGGTTCTCC	600
Db	198	AsnLeuPheLeuProGlnGluCysAlaAenGlyTyrThrSerGlyThrMetGlyPheSer	217
Qy	601	AGTAGTACGGTGACGTTGCTATTGATTCCTCAATATTCATATTCGTTATCACAAAGGA	660
Db	218	ThrAlaGlyThrGlyAlaThrIleAaspCysSerThrValHisValGlyIleSerAenGly	237
Qy	661	TTAAATGATGGAAATATCCGGTTTCATCTGAATCATTTAGTTTACACTAAACTTGTACA	720
Db	238	LeuAenAaspTrpAasnTyrProIleSerSerGluSerPheSerTyrThrIlysThrCysThr	257
Qy	721	TCTAATGGAAATTCAGATTAAATATCAAAATGTACCTGCTGGTTATCGTCCATTATTGAT	780
Db	258	SerThrSerValLeuValThrPheGlnAenValProAlaGlyTyrArgProPheValAasp	277
Qy	781	GCTTATATTTCTGCTACAGATGTTAAACCAATATACCTTTAGCATATATACCAATGATTACT	840
Db	278	AlaTyrIleSerAlaThrArgValSerSerTyrThrMetGlnTyrThrAenIleTyrAla	297
Qy	841	TGTGTCGGCAGTCGCTCGCAAGATGAACCTTTCACTTTAAGATGGAGTCGATACAGAAT	900
Db	298	CysValGlyValAlaAaSerValAaspAaspSerPheThrHisThrTrpArgGlyTyrSerAen	317

Qy	901	AGTGATCCCGGATCAACGGTATGTGCTCACTAAGACAGTGTACAGACAGT	960
Db	318	SerGlnAlaGlySerAsnGlyIleThrIleValValThrThrArgThrValThrAspSer	337
Qy	961	ACCACTGCTGCTCACTACTTTACCAATTCAAATCCAAAGTGTTCATATAAAACCAAAACAATCGAA	1020
Db	338	ThrThrAlaValThrThrLeuProPheAsnSerAspThrAspIysThrIysThrIleGlu	357
Qy	1021	ATTTGCAACCTATTCACACATACATCACAACCTCATATGTTGGTGTGACTACTTCC	1080
Db	358	IleLeuGlnProIleProThrThrIleThrThrSerTyrValGlyValThrThrSer	377
Qy	1081	TATCTGACTAAGACTGACCAAAATGGGTGAACAGCTACTGTTATTGTTGATGTGCCATAT	1140
Db	378	TyrSerThrIysThrAlaProIleGlyGluThrAlaThrValIleValAspValProTyr	397
Qy	1141	CATACTACCACTGTTTACCAGTGAATGGACAGGAAACAATCACTACCACACAACTCGT	1200
Db	398	HisThrThrThrThrValThrThrSerGluTyrThrGlyThrIleThrThrThrThrArg	417
Qy	1201	ACCAATCAACTGATTCGAATGACACAGCTGGTGTGACAGTTCCA	1245
Db	418	ThrAsnProThrAspSerIleAspThrValValValGlnValPro	432
RESULT 7			
ID	ABW01176		
XX	ABW01176 standard; protein; 468 AA.		
AC	ABW01176;		
DT	15-JAN-2004 (first entry)		
DE	Candida albicans agglutinin-like sequence (ALS) 9 protein.		
KW	Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;		
OS	candidiasis; vaccine; fungicide.		
XX	Candida albicans.		
XX	US2003124134-A1.		
PN	03-JUL-2003.		
PD	13-SEP-2002; 2002US-00245802.		
PF	19-NOV-1999; 99US-0166663P.		
PR	18-NOV-2000; 2000US-00715876.		
XX	(HARB-) HARBOR-UCLA RES & EDUCATION INST.		
PA	Edwards JE, Filler SG, Sheppard DC, Ibrahim A, Fu Y;		
XX	WPI; 2003-810971/76.		
XX	N-PSDB; AAD62313.		
XX	New monoclonal antibody against Candida albicans agglutinin-like sequence		
PT	1 adhesin proteins, for use as a vaccine to treat or prevent disseminated		
PT	candidiasis, or to generate an immune response that blocks adherence of		
PT	the organism.		
XX	Disclosure; Page 51-52; 65pp; English.		
PS	The present invention relates to a monoclonal antibody against an		
CC	agglutinin-like sequence (ALS)1 protein that specifically binds an		
CC	epitope in an N-terminal domain and which inhibits adherence of Candida		
CC	albicans to endothelial cells. The invention is useful as vaccines for		
CC	treating and preventing disseminated candidiasis and for generating an		
CC	immune response capable of blocking adherence of the organism. The		
CC	invention is also useful in gene therapy. The present sequence is Candida		
CC	albicans agglutinin-like sequence (ALS) protein		
XX	Sequence 468 AA;		
SQ			

Alignment Scores:
 Pred. No.: 8,91e-139 Length: 468
 Score: 1544.50 Matches: 291
 Percent Similarity: 83.13% Conservative: 54
 Best Local Similarity: 70.12% Mismatches: 69
 Query Match: 67.24% Indels: 1
 DB: 7 Gaps: 1

US-09-715-876-7_COPY_52_1296 (1-1245) x ABW01176 (1-468)

QY	1	AAGACAATCACTGGTGTGTTTTTGA	VAGTGTGTTAAATTCATTAACTTG	TCGTC	CAATGCTGCTAAT	60
DB	18	LysThrIleThrGlyValPheAsnSer	PheAspSerLeuThrTyrThrArgSer	ValGlu	37	
QY	61	TATGCTTTCAAGGCCACAGGATAC	CCCAACTTGGAAATGCTGTTTGGG	TGGTTCCT	TAGAT	120
DB	38	TyrAlaTyrLysGlyProGluThr	ProThrTyrAsnAlaValLeuGly	TyrSerLeu	Asn	57
QY	121	GGTACCAGTGC	CAATCCAGGGGATACATTCAT	TGAATATGCCAT	GTGTGTTTAAAT	180
DB	58	SerThrThrAlaAspProGlyAsp	ThrPheThrLeuIleLeuProCys	ValPheLys	Phe	77
QY	181	ACTACTTCACAAACATCTGTTG	ATTAACTGCGCATGGTGTAAAT	TATGCTACT	TGTGTCAA	240
DB	78	IleThrThrGlnThrSerVal	AspLeuThrAlaAspGlyValSer	TyrAlaThr	CysAsp	97
QY	241	TTTATATCTG	TGAAGAAATTCACAACTTTT	CTCATTAACAT	GTACTGTGACACGCT	300
DB	98	PheAsnAlaGlyGluGluPhe	ThrThrPheSerSerLeuSer	CysThrVal	AsnSerVal	117
QY	301	TTGAAATCAT	CCATTAAGGCATTTGGTACAG	TACTTTACCAAT	TGCAATTCATGCT	360
DB	118	SerValSerTyrAlaArgVal	SerGlyThrValLysLeuPro	IleThrPhe	AsnValGly	137
QY	361	GGAACAGGTT	CATCAACTGATTTTGAAGAT	TTCTAAATGTTT	PACTGCTGTACCAATACA	420
DB	138	GlyThrGlySerSerVal	AspLeuAlaAspSerLys	CysPheThrAla	GlyLysAsnThr	157
QY	421	GTCAATTAAT	GATGGTGATAAGATATCT	CAATGATGTG	AGTTTGAAAGTCAACC	480
DB	158	ValThrPheMetAspGly	AspThrLysIleSerThrThrVal	AspAlaSer	Pro	177
QY	481	GTTGATCCAAGTGCAT	ATTGTTATGCTCTCCAGATTAT	GCCAAAGTCTCAAT	TAAGGTACACA	540
DB	178	ValSerProSerGlyTyr	IleThrSerSerArgIleIlePro	SerLeuAsnLysLeu	Ser	197
QY	541	ACTCTTTTGTGGCACCA	CAATGTGAAAATGGTTATACAT	CTGTGGTAC	ATGGGGTTCTCC	600
DB	198	SerLeuPheValValPro	GlnCysGluAsnGlyTyrThr	SerGlyIleMet	GlyPheVal	217
QY	601	AGTAGTAACGGT	AGCTGCTATTCATGCTCAAA	TATTCATATTTGGT	TATCACAAAGCA	660
DB	218	AlaSerAsnGly---	AlaThrIleAspCysSerAsnVal	AsnIleGlyIleSer	LysGly	236
QY	661	TTAAATGATGCAAT	TATCCGGTTTCATCTGAAT	CATTTAGTTACACT	AAAACTTGTACA	720
DB	237	LeuAsnAspTyrAsn	PheProValSerSerGluSer	PheSerTyrThrLys	ThrCysThr	256
QY	721	TCTAATGGAAT	TACAGATTAAATATCAAAAT	GTACCTGCTGGT	TATCGTCCATTTAT	780
DB	257	SerThrSerIleThrVal	GluPheGlnAsnValPro	AlaGlyTyrArgPro	PheValAsp	276
QY	781	GCTTATATTT	CTGCTACAGATGTTAACCAAT	TATACTTTAGCAT	TATACCAATGATTACT	840
DB	277	AlaTyrIleSerAla	GluAsnIleAspLysTyrThrLeu	ThrThrAla	AsnGluTyrThr	296
QY	841	TCGTGCTGGCAG	CGCTCTGCAAAAGTAAACCT	TTTCACTTAAAGT	ATGGACTGGATACAGAA	900
DB	297	CysGluAsnGlyAsnThr	ValValAspProPheThrLeu	ThrTyrTyrGlyTyr	LysAsn	316
QY	901	AGTGATGCCGG	ATCTAAACGGTATGTCATT	GTGTGTACCACT	AGAACAGTTACAGACGT	960

SQ Sequence 1443 AA;

Alignment Scores:

Pred. No.: 2,78e-134 Length: 1443
 Score: 1500.00 Matches: 281
 Percent Similarity: 81.53% Conservative: 59
 Best Local Similarity: 67.39% Mismatches: 75
 Query Match: 65.30% Indels: 2
 DB: 7 Gaps: 1

US-09-715-876-7_COPY_52_1296 (1-1245) x ABW01173 (1-1443)

QY 1 AAGCAATCACTGCTGTTTGTAGTATTAATTAATCAATGCTGCTCAATGCTGCTAAT 60
 DB 19 LysThrIleSerGlyValPheThrSerPheAsnSerLeuThrThrAsnThrGlyAsn 38
 QY 61 TATGCTTTCAAGCGCCAGGATACCAACTTGGAAATGCTGTTGGTGGTCTCTAGAT 120
 DB 39 TyrProTyrGlyGlyProGlyTyrProThrThrAlaValLeuGlyTyrSerLeuAsp 58
 QY 121 GGTACCAAGTCCCAATCCAGGGATACATTCATTCATGATATGCGATGCTGTTTAAATAT 180
 DB 59 GlyThrLeuAlaSerProGlyAspThrPheThrLeuValMetProCysValPheLysPhe 78
 QY 181 ACTACTTCACAAACATCTGTTGATTAACTCCGATGGTGTAAATATGCTACTTGTCAA 240
 DB 79 IleThrThrGlnThrSerValAspLeuThrAlaAsnGlyValLysTyrAlaThrCysThr 98
 QY 241 TTTTATCTGCTGAAGATACCAACTTTTCTACATTAACATGATGCTGCTGAACGAGCT 300
 DB 99 PheHisAlaGlyGluAspPheThrThrPheSerSerMetSerCysValValAsnAsnGly 118
 QY 301 TTGAATCATCATTAAGGCATTTGGTACAGTACTTACCAATTCATTCATTCATTCAT 360
 DB 119 LeuSerSerAsnIleArgAlaPheGlyThrValArgLeuProIleSerPheAsnValGly 138
 QY 361 GGACAGGTTTCATCACTGATTTGGAAGATCTAAATGTTTACTGCTGCTGACCAATACA 420
 DB 139 GlyThrGlySerSerValAsnIleGlnAspSerLysCysPheThrAlaGlyThrAsnThr 158
 QY 421 GTCATATTATATGATGGTGAATAAGATATCTCAATTTGATGTTGATGTTGAAAGTCAAC 480
 DB 159 ValThrPheThrAspGlyAspHisLysIleSerThrThrValAsnPheProLysThrPro 178
 QY 481 GTTGATCCAGTGCATATTTGATGCTTCACAGATTCACCAAGTCTCAATAAGTCCACA 540
 DB 179 GlnSerSerSerSerSerValTyrPheAlaArgValIleProSerLeuAspLysLeuSer 198
 QY 541 ACTCTTTTGTGGCCACCAATGTGAAATGTTTACATCTGTTACATCTGTTACCAATGCTCC 600
 DB 199 SerLeuValValAlaSerGlnCysThrAlaGlyTyrAlaSerGlyValLeuGlyPheSer 218
 QY 601 AGTAGTAACGGTGAAGTCTTATGATGCTCAATATTCATATTTGATGCTCAACAAAGGA 660
 DB 219 AlaThrLysAspAspValThrIleAspCysSerThrIleHisValGlyIleThrAsnGly 238
 QY 661 TTAATGATGGAATATTCGGTTTCATCTGATTCATTCATTCATTCATTCATTCATTCAT 720
 DB 239 LeuAsnSerTyrAsnMetProValSerSerGluSerPheSerTyrThrLysThrCysThr 258
 QY 721 TCTAATGGAATTCAGATTAATATCAAAATGATGCTGCTGTTATGCTGCTCAATTTATTCAT 780
 DB 259 ProAsnSerPheIleIleThrTyrGluAsnValProAlaGlyTyrArgProPheIleAsp 278
 QY 781 GCTTATATT-----TCTGCTACAGATGTTACCAATATTCATTCATTCATTCATTCAT 834
 DB 279 SerTyrValLysLysSerAlaThrAlaThrAsnGlyPheAsnLeuAsnTyrThrAsnIle 298
 QY 835 TATACTTGTGCTGGCAGTCTGTCGAAAGTAACCTTTCATTCATTCATTCATTCATTCAT 894
 DB 299 TyrAsnCysMetAspGlyLysLysGlyAsnAspProLeuIleTyrPheTyrThrSerTyr 318
 QY 895 AAGATAGTGTGCTGCGGATCTTAACGGTATTGCTGTTGCTGCTGCTGCTGCTGCTGCT 954

DB 319 ThrAsnSerAspAlaGlySerAsnGlyAlaAlaValValValThrThrArgThrValThr 338
 QY 955 GACAGTACCACTGCTGCTCACTACTTTTACCAATCAATCCAAAGTGTGTGATAAAACCAACA 1014
 DB 339 AspSerThrThrAlaIleThrThrLeuProPheAspProThrValAspLysThrLysThr 358
 QY 1015 ATCGAAATTTTGCACACCTATTCCACACCATCAATCAATCAATCAATCAATCAATCAAT 1074
 DB 359 IleGluValIleGluProIleProThrThrThrIleThrThrSerTyrValGlyIleSer 378
 QY 1075 ACTTCTATCTGACTAAGACTGACCAATTTGGTGAACACAGCTACTGTTATTTGATGTG 1134
 DB 379 ThrSerLeuSerThrLysThrAlaThrIleGlyGlyThrAlaThrValValAspVal 398
 QY 1135 CCATATCATACTACCACTGTTTACCAGTGAATGGACAGCAACAACTCACTACCAACACA 1194
 DB 399 ProTyrHisThrThrThrThrIleThrSerIleTyrThrGlySerAlaThrThrSerSer 418
 QY 1195 ACTGCTACCAATCCAACTGATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1245
 DB 419 ThrTyrThrAsnProThrAspSerIleAspThrValValGlnValPro 435
 RESULT 9
 ABW01174
 ID ABW01174 standard; protein; 2297 AA.
 AC ABW01174;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DB Candida albicans agglutinin-like sequence (ALS) 7 protein.
 XX
 KW Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;
 KW candidiasis; vaccine; fungicide.
 XX
 OS Candida albicans.
 XX
 PN US2003124134-A1.
 XX
 PD 03-JUL-2003.
 XX
 PF 13-SEP-2002; 2002US-00245802.
 XX
 PR 19-NOV-1999; 99US-0166663P.
 PR 18-NOV-2000; 2000US-00715876.
 XX
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 PI Edwards JB, Filler SG, Sheppard DC, Ibrahim A, Fu Y;
 XX
 DR WPI; 2003-810971/76.
 DR N-PSDB; AMD62311.
 XX
 PT New monoclonal antibody against Candida albicans agglutinin-like sequence
 PT 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
 PT candidiasis, or to generate an immune response that blocks adherence of
 PT the organism.
 XX
 PS Disclosure; Page 40-45; 65pp; English.
 XX
 CC The present invention relates to a monoclonal antibody against an
 CC agglutinin-like sequence (ALS)1 protein that specifically binds an
 CC epitope in an N-terminal domain and which inhibits adherence of Candida
 CC albicans to endothelial cells. The invention is useful as vaccines for
 CC treating and preventing disseminated candidiasis and for generating an
 CC immune response capable of blocking adherence of the organism. The
 CC invention is also useful in gene therapy. The present sequence is Candida
 CC albicans agglutinin-like sequence (ALS) protein
 XX
 SQ Sequence 2297 AA;
 Alignment Scores:

QY	958	AGTACCACCTGCTGCTACTACTTTTACCATTCAATCCAAAGTGTTCATATAAACCAAAACAATC	101
DB	339	SerIleThrArgThrThrThrLeuProPheIleSerArgLeuGlnLysThrLysThrIle	358
QY	1018	GAATTTTGCACACTATTCCAACTACCATCACAACTTCATATGTTGGTGTGACTACT	1077
DB	359	LeuValLeuGlnProIleProThrThrThrValThrThrSerHisGlyPheAspThr	378
QY	1078	TCCTATCTGACTAAGACTGCGACCAATTTGGTGAACAGCTACTCTTTATTTGTTGATGTGCCA	1137
DB	379	TyrTyrTyrThrLysLysAlaThrIleGlyAspThrAlaThrValPheIleAspValPro	398
QY	1138	TATCATACTACCACAACTGTTTACCAGTGAATGACAGGAAACAATCACTACCAACCAACT	1197
DB	399	GlnHisThrAlaThrThrLeuThrThrTyrTyrGlnGluSerSerThrAlaThrThrThr	418
QY	1198	CGTACCAATCAACTGATTCAATTTGATGACACAGTGGTGGTCAAGTTCCA	1245
DB	419	TyrPheAspAspIleAspLeuValAspThrValIleValLysIlePro	434
RESULT 10			
AAR47575			
ID	AAR47575 standard; protein; 650 AA.		
XX	AAR47575;		
XX			
XX	25-MAR-2003 (revised)		
DT	19-JUL-1994 (first entry)		
XX			
XX	Alpha-agglutinin of Saccharomyces cerevisiae.		
DE			
DE			
XX			
XX			
KW	Immobilisation; enzyme; cell wall; alpha agglutinin; AGA 1; FLO 1;		
KW	Major cell wall protein; glycosyl-phosphatidyl-inositol;		
KW	anchoring protein; alpha factor; alpha-agglutinin; invertase; inulinase;		
KW	alpha-amylase; Saccharomyces cerevisiae; enzymatic process; fermentation;		
KW	biodegradation; catalysis.		
XX			
OS	Saccharomyces cerevisiae.		
XX			
XX			
PN	W09401567-A1.		
XX			
PD	20-JAN-1994.		
XX			
XX	07-JUL-1993; 93WO-EP001763.		
XX			
XX	08-JUL-1992; 92EP-00202080.		
PR			
PR	14-DEC-1992; 92EP-00203899.		
XX			
XX	(UNIL) UNILEVER PLC.		
PA			
PA	(UNIL) UNILEVER NV.		
XX			
PI	Klis FM, Schreuder MP, Toschka H, Verrips CT;		
XX			
XX	WPI; 1994-035071/04.		
DR			
DR	N-PSDB; AAQ54012.		
XX			
PT	Immobilisation of enzymes to microbial cell wall - by prodn. of fusion		
PT	protein of enzyme linked to anchoring protein.		
XX			
PS	Example 1; Page 32-39; 99pp; English.		
XX			
CC	The alpha-agglutinin is used in a method to immobilise enzymes to a		
CC	microbial cell wall. The coding sequence is used in the production of a		
CC	recombinant polynucleotide which comprises a structural gene encoding a		
CC	protein with catalytic activity and at least part of a gene encoding at		
CC	least the C-terminus of a protein capable of anchoring in a eukaryotic or		
CC	prokaryotic cell wall. The anchoring fragment or protein is selected from		
CC	alpha agglutinin, AGA 1, FLO 1, major cell wall protein of lower		
CC	eukaryotes or a proteinase of lactic acid bacteria. The recombinant		
CC	polynucleotide preferably also comprises a sequence encoding a signal		
CC	peptide to ensure secretion of the expressed product. The signal peptide		
CC	is preferably derived from glycosyl-phosphatidyl-inositol, anchoring		
CC	protein, alpha factor, alpha-agglutinin, invertase or inulinase, alpha-		

CC amylase of Bacillus or proteinases of lactic acid bacteria. The host
CC microorganism can be used for performing enzymatic processes on an
CC industrial scale. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 650 AA;

Alignment Scores:

Pred. No.: 3,46e-20 Length: 650
Score: 308.50 Matches: 116
Percent Similarity: 43.33% Conservatives: 79
Best Local Similarity: 25.78% Mismatches: 190
Query Match: 13.43% Indels: 65
DB: 2 Gaps: 20

US-09-715-876-7_COPY_52_1296 (1-1245) x AAR47575 (1-650)

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QY 25 AGTTTAAATCAATTAATGTTGTCCTAAT-----GCTGCTAAATATGCT 66
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 21 AenileAsnAspIleThrPheSerAsnLeuGluIleThrProLeuThrAlaAsn----- 38
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 67 TTCAAGGCCAGGATACCCAACTTGGATGCTGTTTGGGTGGTCTCTTA--GATGGT 123
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 39 ---LysGlnProAsp---GlnGlyTrpThrAlaThrPheAspPheSerIleAlaAspAla 56
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 124 ACCAGTCCCAATCCAGGGGATACATTCACATTAATATGCCATGTGCTTTAAA----- 177
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 57 SerSerIleArgGluGlyAspGluPheThrLeuSerMetProHisValTyArgIleIlys 76
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 178 ---TATACTACTTCAACAACATCTGTTGATTAATCTGCCGATGGTGTAAATATGCTACT 234
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 77 LeuLeuAsnSerSerGlnThrAlaThrIleSerLeuAlaAspGlyThrGluAlaPheIlys 96
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 235 TGTCAATTTTATCTGGTGAA-----GAATTCACAACTTTTCTACATTA 279
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 97 Cys---TyrValSerGlnGlnAlaAlaTyLeuTyLeuTyGluAsnThrPhe----- 112
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 280 ACATGTACTGTGAACAGCGCTTTGAAATCATCCATTAAGGCATTTGGTACAGTACTTTA 339
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 113 ThrCysThrAlaGlnAsnAspLeuSerSerTyAsnThrIleAspGlySerIleThrPhe 132
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 340 CCAATTTGATTCATCAATGTTGGTGAACAGGTTTCATCACTGATTTGGAAAGATCTTAATGT 399
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 133 SerLeuAsnPheSerAspGlySerSerTyGluTyGluLeuGluAsnAlaIysPhe 152
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 400 TTTACTGCTGTACCAATACAGTCACATTTATGATGTGTATGAAGATATCTCAATGAT 459
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 153 PheIysSerGlyProMetLeuValIysLeuGlyAsnGlnMetSerAspVal----- 169
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 460 GTTGAGTTTGAAGAGTCAACCGTTGATCCAACTGTCATAT-----TTGTATGCTTCC 510
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 170 ValAsnPhe-----AspProAlaAlaPheThrGluAsnValPheHisSer 184
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 511 AGAGTTATGCCAAGTCTCAATAAGGTCAACAATCTTTTGTGGCCACCAATGTGMAAAT 570
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 185 GlyArgSerThrGlyTyGlySerPheGluSerTyHisLeuGlyMetTyCysProAsn 204
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 571 GGTACACATCTGGT-----ACAATGGGGTTCCTCCAGTAGTAAGCGTGACGTTGCT 621
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 205 GlyTyPheLeuGlyGlyThrGluIysIleAspTyArgSerSerAsnAsnValAsp 224
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 622 ATTGATTCGCTCAAAATTTCAATATGTTGATTCACAAAAGGATTAATGATTGGAAATTCGCG 681
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 225 LeuAspCysSerValGlnValTySerSerAsnAspPheAsnAspIleThrPhePro 244
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 682 GTTTCATCTGAATCATTTAGTTACACTAAATCTGTACATCTAATGAATTCAGATTAATA 741
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 245 GlnSerTyAsnAspThrAsnAlaAspValThrCysPheGlySerAsnLeuTrpIleThr 264
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 742 TAT---CAAATGTACCTGCTGGTTATCGTCATTTATGATGCTTATATTCT---GCT 795
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 265 LeuAspGluIysLeuTyAspGlyGluMetLeuTrpValAsnAlaLeuGlnSerLeuPro 284
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 796 ACAGATGTTTACCATATCTATTAGCATATACCATGATTATCTTGT----- 843
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Db 285 AlaAsnValaAsnThrIleAspHisAlaLeuGluPheGlnTyThrCysLeuAspThrIle 304
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 844 GCTGGCAGTCTGCTGCAAGTAACCTTTTCACTTTTAAGA-----TGCAGCTGA 891
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 305 AlaAsnThrThrTyAlaThrGlnPheSerThrArgGluPheIleValTyGlnGly 324
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 892 TACAAGAATAGTATGATCCGGATCTAAGCTATTGCTCATTTGTTGTACAACTAGAACAGTT 951
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 325 ArgAsnLeuGlyThrAlaSerAlaIysSerPheIleSerThrThrThrThrAspLeu 344
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 952 ACAGAC-----AGTACCACTGCTGTCACACTTACTTACCAATTCATCAATCCA 993
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 345 ThrSerIleAsnThrSerAlaTySerThrGlySerIleSerThrVal----- 360
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 994 AGTGTTCATAAACCAAAACAAATCGAATTTTGCACCTATTCACCACTACCATCACA 1053
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 GluThrGlyAsnArgThrThrSerGluValIleSerHisValValThrThrSerThrIys 380
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1054 ACTTCATATGTTGGTGTGACTACTTCTATCTGACTAAGACGTGCACCAATTTGGTGAACA 1113
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 381 LeuSerProThrAlaThrThrSerLeuThrIleAlaGlnThrSerIleTySerThrAsp 400
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1114 GCTACTGTTATTTGATGTGCCATATCATCTACTATCACCACA----- 1152
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 401 SerAsnIleThrValGlyThrAspIleHisThrThrSerGluValIleSerAspValGlu 420
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1153 ACTGTTACCACTGATGAGGACAGGACCAATCACTACCACC---ACAACCTGTTACCAATCCA 1209
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 421 ThrIleSerArgGluThrAlaSerThrValValAlaAlaProThrSerThrThrGlyTrp 440
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1210 ACTGATTCAAATTCAGACAGTGGTGGTACAA 1239
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 441 ThrGlyAlaMetAsnThrTyIleProGln 450
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
RESULT 11
ADS43747
ID ADS43747 standard; protein; 650 AA.
XX
AC ADS43747;
XX
DT 02-DEC-2004 (first entry)
XX
DB Bacterial polypeptide #22177.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
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Db 298 SerPheThrSerSerThrValTySerThrAlaSerThrHisThrThrAlaIleThrSer 317
Qy 865 AAACCTTTTCACTTTAAGATGACGTGGATACAAAGAAATAGTATGCGGATCTAAACGGTATT 924
Db 318 ValProThrThrLeu-----GlyThr 324
Qy 925 GTCATTGTTGTACACTAGA----- 945
Db 325 MetValThrSerThrSerArgIleProSerThrValSerThrSerIleProThrSerGln 344
Qy 946 -----ACAGTTTACAGACAGTACCACTGCTGCTCACT---ACTTTACCAATTCATCAACCAAGT 996
Db 345 ProIysThrValAsnSerSerSerGlyGlyIleThrGlySerLeuProMetMetThrAsp 364
Qy 997 GTTGATAAACCAAAACAAATCGAAATTTTGCAACTATTCCAAACCACTACCACTCACACT 1056
Db 365 LeuThrSerGlyTyThrThrValSerSerMetSerAlaIleProThrThrValIleProThr 384
Qy 1057 TCA-----TATGTTGGTGTGACT----- 1074
Db 385 SerLeuThrValGlnAsnThrGluThrSerIlePheValSerMetThrSerAlaThrThr 404
Qy 1075 -----ACT 1077
Db 405 ProSerGlyArgProThrPheThrSerThrValAsnThrProThrArgSerLeuLeuThr 424
Qy 1078 TCCTATCTGACT-----AAGCTGCACCAATTTGGTGAACA 1113
Db 425 SerPheProThrThrHisLeuPheSerSerSerMetSerGluSerSerAlaGlyThrThr 444
Qy 1114 GCTACTGTTATTTGTTGATGTCATATCACTACTACCACTGTT-----ACACGTGAA 1167
Db 445 HisThrGluSerIleSerSerProAlaThrThrSerThrLeuHisThrThrAlaGlu 464
Qy 1168 TGGCAGGAGCAATCACTACCAACCACTCGTACCAATCAACT-----GATTCAATT 1221
Db 465 SerThrProSerCysThrThrThrThrThrSerPheIleThrSerThrThrMetGluProLeu 484
Qy 1222 GACACAGTGGTG 1233
Db 485 SerThrIleVal 488
RESULT 14
ABG66702
ID ABG66702 standard; protein; 1296 AA.
XX AC ABG66702;
XX 30-AUG-2002 (first entry)
XX Human novel polypeptide #37.
XX Human; inflammatory condition; shock; sepsis; immune response; cancer;
KW wound healing; central nervous system disease; haematopoiesis;
KW peripheral nervous system disease; amyotrophic lateral sclerosis; tendon;
KW myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone;
KW cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis;
KW bone degenerative disorder; periodontal disease; reperfusion injury;
KW lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection;
KW allergic condition; thrombolysis; thrombosis; coagulation disorder;
XX fungal infection.
XX Homo sapiens.
XX WO200244340-A2.
XX 06-JUN-2002.
XX 30-NOV-2001; 2001WO-US047004.
XX 30-NOV-2000; 2000US-00728952.
XX
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PA (HYSB-) HYSBQ INC.
XX Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Wang J, Wang D;
PI Yamazaki V, Ujwal ML, Drmanac RT;
XX WPI; 2002-508509/54.
DR N-PSDB; ABK94926.
XX Novel nucleic acids and polypeptides for diagnosis, treatment of
PT inflammatory, autoimmune, nervous system, myeloid or lymphoid cell
PT disorders, cancer and promoting wound healing.
XX Claim 10; Page 604-607; 672pp; English.
XX The invention relates to human novel polynucleotides and associated
CC polypeptides. The polynucleotides and polypeptides are useful for
CC treating inflammatory conditions such as arthritis, nephritis, Crohn's
CC disease, ischaemia-reperfusion injury, shock, sepsis, immune responses
CC and cancer and for promoting wound healing. The sequences are used to
CC induce the proliferation of neural cells and regeneration of nerve and
CC brain tissue, and are useful for the treatment of central and peripheral
CC nervous system diseases and neuropathies, such as Alzheimer's disease,
CC Parkinson's disease, Huntington's disease and amyotrophic lateral
CC sclerosis. The sequences are involved in chemotactic or chemokinetic
CC activity, regulation of haematopoiesis, treatment of myeloid or lymphoid
CC cell disorders and platelet disorders such as thrombocytopenia,
CC regeneration of bone, cartilage, tendon, ligament and/or nerve tissue
CC growth, tissue repair, healing of burns, incisions, ulcers, treatment of
CC osteoporosis, osteoarthritis, bone degenerative disorders and periodontal
CC disease. The sequences of the invention are also useful for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues, immune deficiencies and disorders
CC including severe combined immunodeficiency (SCID), bacterial or fungal
CC infections, autoimmune disorders e.g. multiple sclerosis and myasthenia
CC gravis, allergic conditions such as asthma, thrombolysis or thrombosis
CC and coagulation disorders. Sequences ABG66666-ABG66758 represent human
XX novel polypeptides of the invention
SQ Sequence 1296 AA;
Alignment Scores:
Pred. No.: 1.25e-07 Length: 1296
Score: 179.00 Matches: 116
Percent Similarity: 35.11% Conservative: 68
Best Local Similarity: 22.14% Mismatches: 164
Query Match: 7.79% Indels: 176
DB: 5 Gaps: 24
US-09-715-876-7_COPY_52_1296 (1-1245) x ABG66702 (1-1296)
Qy 4 ACAATCACTGGTGGTTTTGTAGATGTTT-----RATTCATTAACTGGTCCAAT 51
Db 27 ThrIleProSerValArgProThrPheThrSerThrHisAsnThrLeuThrSerSerLeu 46
Qy 52 GCTGCTAATATGCTTTCCAAAGGCCAGGATACCAACTTGGAAATGCTGTTTGGTTGG 111
Db 47 LeuThrThrPhe-----ProGlyThrTyThrSerPheSerSerMetSerAla 62
Qy 112 TCCTTAGATGGTATCC-----AGTGCCAATCCAGGGGATACATTCACA 153
Db 63 SerSerAspGlyThrThrHisThrGluThrIleThrSerLeuProAlaSerThrSerThr 82
Qy 154 TTGAATATGCCATGT-----GTGTTTAATATATACTACTTCA 189
Db 83 LeuHisThrThrAlaGluSerThrThrAlaHisThrThrThrSerPheThrThrSer 102
Qy 190 CAAACA-----TCGTTCATTTAAGTCCGATGGTGTAAATATGCT 231
Db 103 ThrThrMetGluSerProSerSerValAlaThrThrSerThrGly-----Gln 119
Qy 232 ACTTGTCAATTTTATCTCTGGTGAAGAATTCACAACTTTTCTACATTAACATGATCTGTG 291
Db 120 ThrThrPheSerSerSerThrAlaThrPheThrGluThrThrLeuThrThrProThr--- 138
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QY 292 AACGACGCTTTGAAATCATCAATTAAGGCATTTGGTACAGTACTTACCAATTCATTC 351
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 139 ThrAspPheSerGluGluThrLeuThrThrAlaMetThrSerThrProPheThrSer 158
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 352 AATGTTGGTGGAAAGAGTTCATCAACATGATTTGGAAGATTCCTAAAGTTTACTGCTGGT 411
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 159 SerIleThrProThrAsnThrValThrSerMetThrThrMetThrSerTrpProThrAla 178
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 412 ACCAATACAGTCACATTTAATGATGGTGATAAGATATCTCAATGATGGTGGTTGAA 471
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 179 ThrAsnThrLeuSer-----SerLeuThrThrAsnIleLeu 190
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 472 AAGTCAACCGTTGATCCAAGTCAGCATATTTGTATGCTTCCAGAGTTATGCCAAGTCTCAAT 531
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 191 SerSerThrProValProSerThrGluArgThrThrSerHisThr---ThrAsnIleAsn 209
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 532 AAGGTCACAACCTCTTTTGTGGCCACCACCAATGTAATAATGCTTACACATCTGGTACAATG 591
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 210 ProValSerThrLeu----- 214
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 592 GGGTCTCCAGTAGTAACGGTGAGTGTGCTATTGATGCTCAAAATATTCATATTTGGTATC 651
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 215 -----ValThrThrLeuProThrThrIle 222
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 652 ACAAAGGA-----TTAAATGATTGGAATTATCGGTTTCATCTGAATCATTTAGTTAC 705
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 223 ThrArgSerThrProThrSerGluThrThrTyProIleSer----- 237
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 706 ACTAAACCTGTATCATCTAATGGAATTCAGATTAATAATCAAAATGTA----- 753
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 238 ThrSerThrValThrGluSerThrThrGluIleThrTySerThrThrMetThrGluThr 257
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 754 -----CCTGCTGTTATGCTCATTATTGATGCTTATATTTCTGCTACAGAT----- 801
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 258 SerSerSerAlaThrSerLeuProLeuThrSerProLeuValSerThrThrGluThrAla 277
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 802 -----GTTAACCAATATATCTTTA 819
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 278 LysThrProThrThrIleLeuValThrThrThrLysThrThrSerHisSerThrThr 297
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 820 GCATATACCAATGAT-----TATACTTGTGCTGGCAGTCGT-----CTGCAAGT 864
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 298 SerPheThrSerSerThrValTySerThrAlaSerThrHisThrThrAlaIleThrSer 317
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 865 AAACCTTTCATTTAAGATGCGATGCGATACAGAATAGTAGTCGCGATCTAACGGTATT 924
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 318 ValProThrThrLeu-----GlyThr 324
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 925 GTCATTGTTGTACAACACTAGA----- 945
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 325 MetValThrSerThrSerArgIleProSerThrValSerThrSerIleProThrSerGln 344
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 946 -----ACAGTTACAGACAGTACCACCTGCTGTCACT---ACTTTACCATTCATCCAAAGT 996
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 345 ProLysThrValAsnSerSerSerGlyIleThrGlySerLeuProMetMetThrAsp 364
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 997 GTTGATAAACAACCAATCGAAATTTGCAACCTATTCCACCACTACCATCCACCAACT 1056
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 365 LeuThrSerGlyTyThrValSerSerMetSerAlaIleProThrThrValIleProThr 384
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 1057 TCA-----TATGTTGTTGTGACT----- 1074
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 385 SerLeuThrValGlnAsnThrGluThrSerIlePheValSerMetThrSerAlaThrThr 404
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 1075 -----ACT 1077
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 405 ProSerGlyArgProThrPheThrSerThrValAsnThrProThrArgSerLeuLeuThr 424
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 1078 TCCTATCTGACT-----AAGACTGCACCAATTTGGTGAACA 1113
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 425 SerPheProThrThrHisLeuPheSerSerSerMetSerGluSerSerAlaGlyThrThr 444
Db      |||      |||      |||      |||      |||      |||      |||      |||
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QY 1114 GCTACTGTTATTGTTGATGTGCCATATCATATACATCAACACTGTT-----ACCAGTGAA 1167
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 445 HisThrGluSerIleSerSerProAlaThrThrSerThrLeuHisThrThrAlaGlu 464
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 1168 TGGACAGGAGAACATCACTACACCACTCGTACCAATCCCACT-----GATTCAATT 1221
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 465 SerThrProSerCysThrThrThrThrSerPheIleThrSerThrMetGluProLeu 484
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 1222 GACACAGTGGTG 1233
Db      |||      |||      |||      |||      |||      |||      |||      |||
QY 485 SerThrIleVal 488
Db      |||      |||      |||      |||      |||      |||      |||      |||

RESULT 15
ADN18700
ADN18700 standard; protein; 1322 AA.
XX
AC ADN18700;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #1353.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
CAOY(/) CAO Y.
(HINK(/) HINKLE G J.
(SLAT(/) SLATKLE S C.
(CHEN(/) CHEN X.
(GOLD(/) GOLDMAN B S.
Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
WPI; 2004-061375/06.
New recombinant DNA construct comprising a promoter positioned to provide
for expression of a polynucleotide encoding a polypeptide from a
microbial source, useful for producing plants with improved properties.
Claim 1; SEQ ID NO 1353; 122pp; English.
The invention relates to a recombinant DNA construct comprising a
promoter functional in a plant cell, where the promoter is positioned to
provide for expression of a polynucleotide encoding a polypeptide from a
microbial source. The invention also relates to a transformed plant
comprising the recombinant DNA construct and a method of producing a
transformed plant having an improved property. The plant is a crop plant
such as maize or soybean. The method of producing a transformed plant
having an improved property comprises transforming a plant with the
recombinant DNA construct and growing the transformed plant, where the
polynucleotide or polypeptide is useful for improving plant properties.
The recombinant DNA construct is useful for producing plants with
improved plant properties, e.g. improved cold, heat or drought tolerance,
tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
increased resistance to plant disease, better growth rate by modification
of the cell cycle pathway with plant growth regulators, increased rate of
homologous recombination, modified seed oil or protein yield and/or
content, improved yield by modification of carbohydrate, nitrogen or
```

CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 1322 AA;

Alignment Scores:
 Pred. No.: 1.96e-07 Length: 1322
 Score: 177.00 Matches: 112
 Percent Similarity: 34.38% Conservative: 53
 Best Local Similarity: 23.33% Mismatches: 181
 Query Match: 7.71% Indels: 134
 DB: 8 Gaps: 26

US-09-715-876-7_COPY_52_1296 (1-1245) x ADN18700 (1-1322)

Qy 58 AATATGCTTTCAAGGCCAGGATACCAACTTGGATGCTGTTTGGGT---TGGTCC 114
 Db 104 AsnTrpGlyCysLysGlyIleGlyAlaCysSerAsnAsnProIleIleAlaTyrrpSer 123
 Qy 115 TTAGAT-----GGTACCAGTCCCAATCCAGGGATACATTCACATGAATATG----- 162
 Db 124 ThrAspLeuPheGlyPheTyrrThrProThrAsnVal---ThrLeuGluMetThrGly 142
 Qy 163 -----CCATGTGTGTTAAATAATCTACTTCTCAACAACTCT 198
 Db 143 TyrPheLeuProGlnThrGlySerTyrrThrPheLysPheAlaThrValAspAspSer 162
 Qy 199 GTTGATTTAACTGCGGAGGT---GTTAAATATGCTACTTCTCAATTTATCTGGTGAA 255
 Db 163 AlaIleLeuSerValGlyGlySerIleAlaPheGluCysCys-----AlaGln 178
 Qy 256 GAATTCACAACTTTTTCACATTAACATGACTGTGAACGACGCTTGGAAATCATCCATT 315
 Db 179 GluGlnProIleThrSerThrAsnPheThrIleAsn-----GlyIle 193
 Qy 316 AAGGCATT-----GGTACAGTT----- 333
 Db 194 LysProTrpAsnGlySerProProAspAsnIleThrGlyThrValTyrrMetTyrAlaGly 213
 Qy 334 -----ACTTACCAATT 345
 Db 214 PheTyrrProMetLysIleValTyrrSerAsnAlaValAlaTrpGlyThrLeuProIle 233
 Qy 346 GCATTCATGTT---GGTGGAAACAGTTTCATCACTGATTTGGAGATTCTAAATGTTTT 402
 Db 234 SerValThrLeuProAspGlyThrThrValSerAspPheGluGly----- 249
 Qy 403 ACTGCTGTACCAATACAGTCACATTAATGATGGTGAATAAGATATCTCAATTGATGTT 462
 Db 250 -----TyrValTyrrThrPhe-----AspAsnAsnLeuSer----- 259
 Qy 463 GAGTTTGAAGAGTCAACCGTTGATCCAAAGTCATATTTGTATGCTTCCAGATGATGCA 522
 Db 260 GlnProAsnCysThrIleProAspProSerAsnTyrrThr---ValSerThrThrIleThr 278
 Qy 523 AGTCTCAATAGGTCAACAACCTCTTTTGTGGCACCACCAATGTGAAATGGTTACACATCT 582
 Db 279 ThrThrGluProTrpThrGlyThrPheThrSerThrSerThrGluMetThrThrValThr 298
 Qy 583 GGTACAAATGGGCTCTCCAGTAGTAACGGTGAAGTGTGCTATTGATTTGCTCAAAATATCAT 642
 Db 299 GlyThrAsnGlyValProThrAspGluThrValIleValIleArgThrProThrThrAla 318
 Qy 643 ATTGGTATCAGAAAAGGATTAATGATTTGGAATATCCGGTTTCACTGAATCATTTAGT 702
 Db 319 SerThrIleIleThrThrThrGluProTrpAsnSerThrPheThrSerThrSerThrGlu 338
 Qy 703 TACACTAAACTTGTACATCTAATCGAATTCAGATTAAATATCAAAATGTACCTGCTGCT 762

Db 339 LeuThrThrValThrGlyThrAsnGlyValArgThrAspGluThrIleIle--- 355
 Qy 763 TATCGTCCATTTATTCATGCTTATATTTCTGCTACAGATGTTAAACCAATATATCTTTAGCA 822
 Db 356 -----ValIleArgThrProThrThrAlaThrThrAlaIleThrThrGluPro 372
 Qy 823 TATACCAATGATTTATCTGCTGCGCAGTCGCTGCAAAAGTAAACCTTTTCACTTTAAGA 882
 Db 373 TrpAsnSerThrPheThrSerThrSerThrGluLeu----- 384
 Qy 883 TGGACTGGATACAGAATACTGATGCGGATCTAAACGGTATT-----GTCATTGTT 933
 Db 385 -----ThrThrValThrGlyThrAsnGlyLeuProThrAspGluThrIle 399
 Qy 934 GCTACAACATAGAACAGTTACAGACAGTACCACCTGCTGCTACTACTTTA---CCATTCAT 990
 Db 400 IleValIleArgThrProThrThrAlaThrThrAlaMetThrThrThrGlnProTrpAsn 419
 Qy 991 CCAAGTGTTCATAAAACCAAAACA----- 1014
 Db 420 AspThrPheThrSerThrSerThrGluLeuThrThrValThrGlyThrAsnGlyLeuPro 439
 Qy 1015 -----ATCGAAATTTTGCACCTTATCCAAACCACTACATCACAACCT--- 1056
 Db 440 ThrAspGluThrIleIleValIleArgThrProThrThrAlaThrThrAlaMetThrThr 459
 Qy 1057 -----TCATATGTTGGTGTGACTACTTCTATCTGACTTAACACTGCA 1098
 Db 460 ThrGlnProTrpAsnAspThrPheThrSerThrSerThrGluLeuThrThrValThrGly 479
 Qy 1099 -----CCAATTGGTGAACACAGCTACTGTTATTGTTGATGTCCTATATCATCTACT 1146
 Db 480 ThrAsnGlyLeuProThrAspGluThr---IleIleValIleArgThrProThrThrAla 498
 Qy 1147 ACCACA-----ACTGTTACAGTGAATGGACAGGAACAATCACT----- 1185
 Db 499 ThrThrAlaMetThrThrThrGlnProTrpAsnAspThrPheThrSerThrSerThrGlu 518
 Qy 1186 ---ACCACACACACTCGTACCAT-----CCAATGATTCAATTTGACACAGTGGTGGTA 1236
 Db 519 IleThrThrValThrGlyThrAsnGlyLeuProThrAsp-----GluThrIleIleVal 536

Search completed: September 8, 2005, 17:41:09
 Job time : 227 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 08:52:54 ; Search time 3078 Seconds
(without alignments)
15396.366 Million cell updates/sec

Title: US-09-715-876-7_COPY_52_1296

Perfect score: 1245

Sequence: 1 aagacaatcactggtgtttt.....cagtgggtggtacaagtcca 1245

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1.*
2: gb_est2.*
3: gb_hcc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_g881.*
9: gb_g882.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	155	12.4	1047	9	CNS07D6L	AL440083 T7 end of
2	152.8	12.3	560	6	CD085816	CD085816 MCI-0021p
3	139.4	11.2	1011	9	CNS07DAY	AL440240 T7 end of
C 4	121.2	9.7	1050	9	CNS07CMQ	AL439368 T7 end of
5	82.6	6.6	525	8	BZ351620	BZ351620 hw04f06.g
C 6	80.4	6.5	735	9	CNS04NSM	AL299119 Tetraodon
7	80.2	6.4	843	8	BZ643413	BZ643413 OGAW57TM
8	78.4	6.3	501	9	FR0048173	AL444958 Fugu rubr
9	77.8	6.2	619	9	CG372306	CG372306 OG4B108TC
10	77.6	6.2	513	8	BZ423698	BZ423698 id52c10.g
11	76.6	6.2	773	9	CNS01VTG	AL169549 Tetraodon
12	75.8	6.1	480	8	BZ643398	AL169549 OGAW57TC
13	75.2	6.0	694	8	BH355163	BH355163 CH230-81p
14	71.8	5.8	494	9	FR0048073	AL444858 Fugu rubr
C 15	69.8	5.6	427	8	BZ422321	BZ422321 id52c10.b
16	69.6	5.6	350	8	BH879665	BH879665 ht47hl2.g
17	69.6	5.6	989	9	CNS02HA4	AL197365 Tetraodon
18	68.6	5.5	334	8	BZ614791	BZ614791 ig46f04.g
19	68.4	5.5	395	8	BZ316940	BZ316940 ia78dl2.b
20	67.8	5.4	989	8	CC149236	CC149236 ZMBB001
21	67.6	5.4	356	8	CC171914	CC171914 ii74fl2.g
22	66.8	5.4	699	5	BK729701	BK729701 BX729701
23	66.6	5.3	423	8	BZ309688	BZ309688 ic10c08.b
24	66.6	5.3	933	8	AZ204694	AZ204694 SP_0100_A

C 25	65.8	5.3	530	8	AZ166409	AZ166409 SP_0088_A
26	65.4	5.3	306	8	BZ375744	BZ375744 ie61b04.g
C 27	65	5.2	528	6	CD336470	CD336470 StrPus37.
28	64.8	5.2	311	8	BZ638753	BZ638753 OGCAx82TM
29	64.6	5.2	320	8	BZ314341	BZ314341 h216b12.b
30	64	5.1	305	8	BZ333772	BZ333772 hx72h02.g
31	63.6	5.1	428	5	BQ036742	BQ036742 SS2-0450
32	63.4	5.1	621	8	AZ164800	AZ164800 SP_0076_B
33	62.6	5.0	914	8	AZ205202	AZ205202 SP_0100_A
C 34	62.4	5.0	810	8	AZ199472	AZ199472 SP_1039_B
35	62.2	5.0	788	8	AZ183942	AZ183942 SP_1002_B
36	62	5.0	280	9	CG218306	CG218306 OGTX57TH
37	61.8	5.0	266	8	BZ313584	BZ313584 h209b05.b
38	61.6	4.9	287	8	BZ644508	BZ644508 OGCBP93TM
39	61.2	4.9	619	9	FR0047601	AL444386 Fugu rubr
40	60.8	4.9	550	9	FR0043207	AL130699 Fugu rubr
41	60.4	4.9	450	9	FR0025683	AL018519 F. rubripe
42	59.8	4.8	922	7	CK411084	CK411084 AUF_1phdk
43	59.6	4.8	320	8	CC167070	CC167070 i158a04.g
C 44	59.4	4.8	469	9	CL569187	CL569187 4-12-4 Ma
45	59.4	4.8	798	2	BF936821	BF936821 EST459876

ALIGNMENTS

RESULT 1	CNS07D6L/c	CNS07D6L	1047 bp	DNA	linear	GSS 08-JUL-2001
LOCUS	T7 end of clone BD0AA009H06 of library BD0AA	T7 end of clone BD0AA009H06 of library BD0AA	from strain CBS 94 of			
DEFINITION	Candida tropicalis, genomic survey sequence.	Candida tropicalis, genomic survey sequence.				
ACCESSION	AL440083	AL440083	1 GI:12223494			
VERSION	GSS	GSS				
KEYWORDS	Candida tropicalis	Candida tropicalis				
SOURCE	Candida tropicalis	Candida tropicalis				
ORGANISM	Candida tropicalis	Candida tropicalis				
REFERENCE	1 (bases 1 to 1047)	1 (bases 1 to 1047)				
AUTHORS	Souciat,J.L., Aigle,M., Artiguenave,P., Blandin,G., Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekala,P., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissbach,J.	Souciat,J.L., Aigle,M., Artiguenave,P., Blandin,G., Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekala,P., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissbach,J.				
TITLE	Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies	Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies				
JOURNAL	FEBS Lett. 487 (1), 3-12 (2000)	FEBS Lett. 487 (1), 3-12 (2000)				
MEDLINE	20584711	20584711				
PUBMED	11152876	11152876				
REFERENCE	2 (bases 1 to 1047)	2 (bases 1 to 1047)				
AUTHORS	Blandin,G., Ozier-Kalogeropoulos,O., Wincker,P., Artiguenave,P. and Dujon,B.	Blandin,G., Ozier-Kalogeropoulos,O., Wincker,P., Artiguenave,P. and Dujon,B.				
TITLE	Genomic exploration of the hemiascomycetous yeasts: 16. Candida tropicalis	Genomic exploration of the hemiascomycetous yeasts: 16. Candida tropicalis				
JOURNAL	FEBS Lett. 487 (1), 91-94 (2000)	FEBS Lett. 487 (1), 91-94 (2000)				
MEDLINE	20584726	20584726				
PUBMED	11152891	11152891				
REFERENCE	3 (bases 1 to 1047)	3 (bases 1 to 1047)				
AUTHORS	Genoscope.	Genoscope.				
TITLE	Direct Submission	Direct Submission				
JOURNAL	Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. [E-mail : seqref@genoscope.cns.fr Web : http://www.genoscope.cns.fr]	Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. [E-mail : seqref@genoscope.cns.fr Web : http://www.genoscope.cns.fr]				
COMMENT	This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of	This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of				

KEYWORDS GSS.
SOURCE Candida tropicalis
ORGANISM Candida tropicalis

REFERENCE Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
AUTHORS 1 (bases 1 to 1011)
Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)

JOURNAL MEDLINE
PUBMED 20584711
REFERENCE 11152876
AUTHORS 2 (bases 1 to 1011)
Blandin,G., Ozier-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
Dujon,B.
Genomic exploration of the hemiascomycetous yeasts: 16. Candida
tropicalis
FEBS Lett. 487 (1), 91-94 (2000)

JOURNAL MEDLINE
PUBMED 20584726
REFERENCE 11152891
AUTHORS 3 (bases 1 to 1011)
Genoscope.
Direct Submission
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. [E-mail :
seqref@genoscope.cns.fr - Web :
this GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 Kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.

FEATURES
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/note="similar to P46590 [Agglutinin-like protein 1
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1 putative frameshift(s)"
/evidence=not_experimental

ORIGIN
Query Match 11.2%; Score 139.4; DB 9; Length 1011;
Best Local Similarity 65.0%; Pred. No. 7.9e-24;
Matches 214; Conservative 4; Mismatches 110; Indels 1; Gaps 1;
QY 1 AAGACAATCACTGGTGTGTTTGGATGATGTTTAACTTAACCTGGTCCCAATGCTGCTAAT 60
DB 670 AAAGAAATTCGCGGTGTGTTTATAGGATTTGAATCTTAACTGGGATGAAGCGTGGTAAAT 729
QY 61 TATGCTTTCAAGGCCAGGATACCACCTGGATGCTGTTTGGTGGTTCCTTAGAT 120
DB 730 TATGCATATCAAGGTCCTCAATATCCACATGGAATGCGGTGTTGATGTTGCTTAGAT 789
QY 121 GGTACCAAGTGGCAATCCAGGGGATACATTCACATTTGAATATGCCAATGTTGTTAAATAT 180
DB 790 GGCAACAACAACATCCCAGGTGATAGGTTCACTTTGATCATGCCCTGCTCTTCAAGTTC 849

QY 181 ACTACTTCAAAACATCTGTGTGATTTAACTGCGATGGTGTAAATGATGCTACTTGTCAA 240
DB 850 ACTAGCTTTCGATVTTCTGTTGGATCTGACTGCAATGGKATGACATATGCCACATGTGAT 909
QY 241 TTTTAT-TCGGTGAAGAAATTCACAACTTTTCTACATTTAATGCTACTGTGAACGACGC 299
DB 910 CTTTCATGCKKGGTGAAGATTTACTACTTCTAGTTTACGCTGCTACTGCTAYAGATTC 969
QY 300 TTGAAATCATCCATTAAGGCAATTTGGTA 328
DB 970 GTTAAGTCTGTTTCATGAGCTATGGGATA 998

RESULT 4
CNS07CMQ 1050 bp DNA linear GSS 08-JUL-2001
LOCUS T7 end of clone BD0AA004B02 of library BD0AA from strain CBS 94 of
DEFINITION Candida tropicalis, genomic survey sequence.
ACCESSION AL439368
VERSION AL439368.1 GI:12222781
KEYWORDS GSS.
SOURCE Candida tropicalis
ORGANISM Candida tropicalis

REFERENCE Rukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
AUTHORS 1 (bases 1 to 1050)
Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)

JOURNAL MEDLINE
PUBMED 20584711
REFERENCE 11152876
AUTHORS 2 (bases 1 to 1050)
Blandin,G., Ozier-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
Dujon,B.
Genomic exploration of the hemiascomycetous yeasts: 16. Candida
tropicalis
FEBS Lett. 487 (1), 91-94 (2000)

JOURNAL MEDLINE
PUBMED 20584726
REFERENCE 11152891
AUTHORS 3 (bases 1 to 1050)
Genoscope.
Direct Submission
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. [E-mail :
seqref@genoscope.cns.fr - Web :
this GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 Kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.

FEATURES
source
1..1050
/organism="Candida tropicalis"
/mol_type="genomic DNA"
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/db_xref="taxon:5482"
/clone="BD0AA004B02"
/clone_lib="BD0AA"
/note="end : 77"
misc_feature
/note="similar to O13368 [Agglutinin-like protein ALA1
precursor] [Candida albicans]"

AUTHORS	Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C., Fzames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,C., Bernot A. and Weissenbach,J.
TITLE	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL	Genome Res. 10 (7), 939-949 (2000)
MEDLINE	20359837
PUBMED	10899143
REFERENCE	3 (bases 1 to 735)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : secref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT	This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/tetraodon .
FEATURES	Location/Qualifiers
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	/note="Genoscope sequence ID : COBG123AG03LP1-end : T7"

[illegible]

RESULT 7	BZ643413/c	LOCUS	BZ643413	843 bp	DNA	linear	GSS 29-JAN-2003
		DEFINITION	OGAOW57TM	ZM 0.7 1.5 KB	zebra mays	genomic clone	ZMMBMA0111J17,

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

genomic survey sequence.
BZ643413
BZ643413.1 GI:28104915
GSS.

REFERENCE SOURCE ORGANISM	REFERENCE AUTHORS	TITLE JOURNAL COMMENT
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100	100	100

genomic survey sequence.
 BZ643413
 BZ643413.1 GI:28104915
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 Zea mays
 Zea mays
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 843)
 Whiteclaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
 Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
 Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

ORIGIN

Query Match	6.4%	Score 80.2;	DB 8;	Length 843;
Best Local Similarity	45.7%;	Pred. No. 5e-09;		
Matches 280;	Conservative 0;	Mismatches 333;	Indels 0;	Gaps 0;
QY	616	GTTCGCTATTGCTGCTCAAAATATTCATATATTTGGTATCACAAAGGATTAATGATTGGAAT	675	
Db	792	GCTACTACTGCTACTACTGCTGCTGATGCTACTGCTACTGCTACTGCTACTGCTACT	733	
QY	676	TATCCGCTTTCATCTGAAATCATTTAGTTACATAAAACCTTGTCATCTTAATGGAATTCAG	735	
Db	732	ACTGCTACTGCTGCTACTGCTACTGCTGCTACTACTACTGCTACTGCTACT	673	
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Db	672	ACTACTGCTACTGCTGCTACTACTACTACTGCTACTGCTACTGCTACTGCTGCT	613	
QY	796	ACAGATGTTAACCAATATATCTTTAGCATATACCAATGATTAATCTTGTGCTGCGACGTCGT	855	
Db	612	ACTGCTGCTATTGCTGCTACTCTCCAGCTACTACTGCTGTTGCTGCTACTGCTGCTACT	553	
QY	856	CTGCAAAAGTAAACCTTTTCACCTTTTAAGATGACCTGGATACAAAGTAATAGTCGATCGCGATCT	915	
Db	552	GCTACTGCTGCTACTGCTGCTGCTACTACTGCTGCTACTGCTGCTACTGCTACTACTACT	493	
QY	916	AACGGTATTGCTATTGTTGTACAACTAGAACAGTTACAGACAGTACCACTGCTGTCACCT	975	
Db	492	GCTACTACTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTACTACTACT	433	
QY	976	ACTTTACATTCATTCGAGTGTGATTAACCAAAACAATCGAAATTTTGGCAACCTATT	1035	
Db	432	GCTGCTGCTACTACTACTGCTAAATGCTACTACTACTACTGCTGCTACTACTACTACTACT	373	
QY	1036	CCAACTACTACCATCAAACTTCATATGTTGGTGTGACTACTTCTCTATCTGACTAAGACT	1095	
Db	372	GCTCCTACTACTGCTACTGCTACTGCTACTGCTTCTACTACTACTACTGCTACTGCTACTGCT	313	
QY	1096	GCACCAATTTGGTGAACACGCTACTGTTATTGTTGATGTGCTGCATATCATACTACCACAACT	1155	

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Db      312 ACTGCTACTGCTACAGCTACTACAGCTACTACTGCTACTCTGCTACTGCTACT 253
Qy      1156 GTTACCGTGAATGGACGAGCAATCAGTACACCACTGTTACCAATCAACTGAT 1215
Db      252 ACTACTACTGCTACTACTGCTACTACTACTGCTACTACTGCTACTACTGCTACTGCT 193
Qy      1216 TCAATTGACACAG 1228
Db      192 ACTGCTGCTACTG 180

RESULT 8
LOCUS   PR0048173          501 bp      DNA      linear      GSS 05-JAN-2001
DEFINITION Fugu rubripes GSS sequence, clone 264E22ca9, genomic survey
sequence.
ACCESSION AL444958      GI:12053458
VERSION   AL444958.1
KEYWORDS  GSS; genome survey sequence.
SOURCE   Takifugu rubripes (Fugu rubripes)
ORGANISM Takifugu rubripes
          Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
          Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
          Acanthomorphia; Acanthopterygii; Percomorpha; Tetraodontiformes;
          Tetraodontidae; Tetraodontidae; Takifugu.
REFERENCE 1 (bases 1 to 501)
AUTHORS  Clark,M.S.
          Direct Submission
          Submitted (29-SEP-2000) MRC Human Genome Mapping Project Resource
          Centre Hinxton, Cambridge, CB10 1SB. UK Email:
          biohelp@hmp.mrc.ac.uk
COMMENT  Vector: pBluescript II KS
          V-type: phagemid
          PRIMER: KS
DESCR:   One pass dye-terminator sequencing of BAC (pBelobACII) cloned
          genomic sequence
          The BACs can be obtained from http://www.incyte.com.

FEATURES             source
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ORIGIN
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Matches 226; Conservative 0; Mismatches 246; Indels 0; Gaps 0;

Qy      755 CTGCTGTTATCGGCCATTTATGATGCTTATATTTCTGCTACAGATGTTAACCAATATA 814
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Qy      815 CTTTAGCATACCAATGATATATCTTGTGCTGCAGTCGCTCGCAAGTAAACCTTTCA 874
Db      79 CTACTACTACTACTGCTACTACTACTACTGCTACTACTACTACTACTACTACTACTGCTG 138
Qy      875 CTTTAAAGTACTGCTGATACAGAAATGATGATGCGGATCTAAACGGTATTGTCTATTGTG 934
Db      139 CTGCTTCTACTACTGCTACTACTACTACTACTGCTACTACTACTGCTGCTTCTACTACTA 198
Qy      935 CTACAACTAGAAAGTTACAGACAGTACCACTGCTGTGTCATCTATTACCATTCATCAAA 994
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Qy      995 GTGTTGATAAAACCAAAACCAATCGAAATTTTGCAACCTATTTCCAACCACTACCATCAAA 1054
Db      259 CTACTACTACTACTGCTGCTACTACTACTACTGCTACTACTACTACTACTACTACTGCT 318
Qy      1055 CTTTCATATGTTGGTGTGACTACTTCTCTATCTGACTAAAGCTGCACCAATTGGTGAACAG 1114
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Db      319 CTTTCTACTACTACTACTACTACTACTACTACTACTACTACTACTGCTGCTTCTACTACTGCTA 378
Qy      1115 CTACTGTTATTTGTTGATGGCCATATCATACTACTACCACTGTTACCACTGAATGGACAG 1174
Db      379 CTACTACTACTACTACTACTACTACTACTGCTACTACTACTACTACTACTACTGCTACTACTG 438
Qy      1175 GAACAATCACTACCACCACTCGTACCAATCCAACTGANTCAATTTGACAC 1226
Db      439 CTGCTACTACTACTACTACTACTGCTAGTAGTACTACTACTACTACTACTACTAGTACTAC 490

RESULT 9
LOCUS   CG372306          619 bp      DNA      linear      GSS 26-AUG-2003
DEFINITION OG4BI087C ZM 0.7 1.5 KB Zea mays genomic clone ZMBMa0811B15,
genomic survey sequence.
ACCESSION CG372306
VERSION   CG372306.1 GI:34289573
KEYWORDS  GSS.
SOURCE   Zea mays
ORGANISM Zea mays
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 619)
AUTHORS  Whitelaw,C.A.; Quackenbush,J.; Van Aken,S.; Utterback,T.;
          Resnick,A.; Fraser,C.M.; Budiman,M.A.; Bedell,J.A.; Rohlfing,T.;
          Citek,R.W.; Nunberg,A.; Robbins,D. and Lakey,N.
          Consortium for Maize Genomics
          Unpublished (2002)
          Contact: Cathy Whitelaw
          TIGR
          9712 Medical Center Drive, Rockville, MD 20850, USA
          Tel: 301-838-5843
          Fax: 301-838-0208
          Email: whitelaw@tigr.org
          Seq primer: TF
          Class: sheared ends.

FEATURES             source
          source
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Matches 226; Conservative 0; Mismatches 247; Indels 0; Gaps 0;

Qy      750 TGTACCTGCTGTTATCGTCCATTATTATGATGCTTATATTTCTGCTACAGATGTTAACCA 809
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Db      173 TACTACTACTACTACTACTACTACTACTACTGCTGCTGCTGCTGCTACTACTACTACTGCTG 232
Qy      930 TGTGTTCAAACTAGAACAGTTACAGACAGTACCACTGCTGTGTCATCTACTTTTCAATTCAA 989
Db      233 TACTACTACTGCTACAACTACTCTGCTACTACTACTACTGCTACTACTACTACTACTACTACTAC 292
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ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
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		GSS.	Zea mays	Clade: Panicoidae; Andropogoneae; Zea.

SOURCE

Rattus norvegicus

ORGANISM *Rattus norvegicus*
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 694)
 AUTHORS Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
 Shvartsbeyn, A., Gebregorgis, E., Overton, L., Russell, D., Chen, D.,
 Riggs, P., de Jong, P. and Fraser, C.M.
 TITLE Rat BAC End Sequences from Library CHORI-230 EcoRI segment
 JOURNAL Unpublished (1999)
 COMMENT Other GSSs: CH230-81P6-TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the rat BAC library CHORI-230
 (http://www.chori.org/bacpac/rat230.htm). For BAC library
 availability, please contact Pieter de Jong (pdejong@mail.cho.org).
 Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/or_ering_information.htm). BAC end
 plate: http://www.tigr.org/tldb/bac_ends/rat/bac_end_intro.html
 Plate: 81 row: P column: 6
 Seq primer: SP6
 Class: BAC ends.
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 CHORI-230 Rat (BN/SnHsd/MCW) BAC library produced by
 Pieter de Jong"

ORIGIN
 Query Match 6.0%; Score 75.2; DB 8; Length 694;
 Best Local Similarity 48.2%; Pred. No. 8.6e-08;
 Matches 241; Conservative 0; Mismatches 258; Indels 1; Gaps 1;
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 DB 192 AGCAGCAGTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTAA 251
 QY 747 AAATGTACTGCTGTTATCGTCCATTTTATTGATGCTTATATTTCTGCTACAGATGTTAA 806
 DB 252 TAATATTACTACTACAAGTACTACTATCATCTAC-TACACTACTATTACTACTACTAC 310
 QY 807 CCAATATCTTTAGCATATACCAAGTATTATATTTGTCGTGCGAGTCGTCTGCAAGTAA 866
 DB 311 TAAAACTACTACTACTAATAATAATATTTACTACTACTACAAGTACTACTATTAATCTAC 370
 QY 867 ACCTTTCTCTTTAAGATGAGCTGGATACAAGAAATAGTATGCCGGATCTAAACGGTATTGT 926
 DB 371 TACTACTACTACTATTACTGCTACTACTACAAGTACTACTATTATTCTGCTGTACAATAC 430
 QY 927 CATTTGTTGTTACACTAGAACAGTTACAGAGTACCACTGCTGTCTACTTTTACCATT 986
 DB 431 TACTATTACTACTACAACACTACTACTACTAAAACTACTACTATTACTACTACTACAAC 490
 QY 987 CAATCCAGTGTGTATAAACCAACCAATCGAAATTTTGCAACCTATTTCACCACTAC 1046
 DB 491 TACTACTCTGTTATTACTACTACTAAACTACTACTATTACTACTACTATTACTATTAT 550
 QY 1047 CATCAAACTTCATATGTTGGTGTGACTACTTTCCTATCTGACTAAGACTGCACCAATTTGG 1106
 DB 551 TACTACTACTACAAGTACTACTATTACTACTACTATTACTACTACTACTACTACTAT 610

QY 1107 TGAACAGCTACTGTTATTGTTGATGTCGATATCATATCTACTACCACAACTGTTTACCAGTGA 1166
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 DEFINITION sequence.
 ACCESSION AL444858.1 GI:12052694
 KEYWORDS GSS; genome survey sequence.
 WORDS Takifugu rubripes (Fugu rubripes)
 SOURCE Takifugu rubripes
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 Tetraodontidae; Tetraodontidae; Takifugu.
 REFERENCE 1 (bases 1 to 494)
 AUTHORS Clark, M.S.
 TITLE Direct Submission
 JOURNAL Submitted (29-SEP-2000) MRC Human Genome Mapping Project Resource
 Centre Hinxton, Cambridge, CB10 1SB. UK Email:
 biohelp@hmp.mrc.ac.uk
 COMMENT Vector: pBluescript II KS
 V type: phagemid
 PRIMER: KS
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 One pass dye-terminator sequencing of BAC (pBelobACII) cloned
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 The BACs can be obtained from http://www.incyte.com.
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ORIGIN
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 Best Local Similarity 47.1%; Pred. No. 5.7e-07;
 Matches 220; Conservative 0; Mismatches 247; Indels 0; Gaps 0;
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 QY 815 CTTTTCATATACCAATGATTATCTTGTGTCGACGTCGTCGCAAGTAAACCTTTCA 874
 DB 85 CTACTGCGACGACGCTACTACTACTGCGGCTGCTTCTACTACTGCTACTACTACGA 144
 QY 875 CTTTAAAGTAGGACTGGATACAAGAAATAGTAGTGGGATCTAACGGTATTGCTATTGTTG 934
 DB 145 CGACTGCTACTACTACTACTGCTACTACTACTACTACTACTACTACTACTACTACTA 204
 QY 935 CTACAACCTAGAAACAGTTACAGACAGTACCTGCTGCTACTTTTACCAATCAATCCAA 994
 DB 205 CTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTA 264
 QY 995 GTGTTGATAAACCAAAACAAATCGAAATTTTGCAACCTATTTCACCACTACCAACAA 1054
 DB 265 CTACTACTACTACTACTACTGCTACTGCTACTACTACTACTACTACTACTACTACTA 324
 QY 1055 CTTTCATATGTTGGTGTGACTACTTTCCTATCTGACTAAGACTGCACCAATTTGGTGAACAG 1114
 DB 325 CTACTACTACTACTGCTGCTACTGCTGCTACTACTACTACTACTACTACTACTACTA 384

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 11:49:20 ; Search time 1814 Seconds
(without alignments)

4090.060 Million cell updates/sec

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Perfect score: 1245

Sequence: 1 aagacaatcactggtgtttt.....cagtggtggtacagtcca 1245

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5552208 seqs, 2979665951 residues

Total number of hits satisfying chosen parameters: 11104416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	947.4	76.1	3360	15	US-10-245-802-11
5	895	71.9	1404	15	US-10-245-802-9
6	733.4	58.9	1407	15	US-10-245-802-13
7	713.8	57.3	1404	15	US-10-245-802-23
8	574.6	46.2	4332	15	US-10-245-802-17
9	393.6	31.6	6897	15	US-10-245-802-19
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					Sequence 15, Appl
					Sequence 21, Appl
					Sequence 11, Appl
					Sequence 9, Appl
					Sequence 13, Appl
					Sequence 23, Appl
					Sequence 17, Appl
					Sequence 19, Appl
					Sequence 2885, Ap

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	17	45.6	3.7	32392	19	US-10-706-635-27	Sequence 27, Appl
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	28	43.8	3.5	1521	18	US-10-741-387-160	Sequence 160, App
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ALIGNMENTS

RESULT 1

US-10-245-802-7
; Sequence 7, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 7
; LENGTH: 3786
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-245-802-7

Query Match 100.0%; Score 1245; DB 15; Length 3786;
Best Local Similarity 100.0%; Pred. No. 2.2e-272;
Matches 1245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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US-10-245-802-15
; Sequence 15, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 3813
; TYPE: DNA
; ORGANISM: Candida albicans
; US-10-245-802-15

Query Match 84.1%; Score 1046.6; DB 15; Length 3813;
Best Local Similarity 90.0%; Pred. No. 2.8e-227;
Matches 1121; Conservative 0; Mismatches 124; Indels 0; Gaps 0;
Qy 1 AGACAATCACTGCTGTTTTCATAGTTTAAATTCATTAACCTGGTCCAAATGCTGCTAAT 60
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Qy 61 TATGCTTTCAAAGGGCCAGGATACCCAACTTCGGAATGCTGTTTGGGTTGGTCTTTAGAT 120
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Qy 781 GCTTATATTTCTGCTACAGATGTTAAACCAATATATCTTTAGCATATACCAATGATTATACT 840
Db 832 GCTTATATTTCTCCTCAGATAATACCAAGTATCAATTTGCTATATAAAATGACTATACT 891
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Db 1252 ACCAATCCACTGATTCAATTTGACACAGTGGTGGTGTACAAAGTTCCA 1296

RESULT 3

US-10-245-802-21
; Sequence 21, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 4383
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-245-802-21

Query Match 76.2%; Score 949; DB 15; Length 4383;
Best Local Similarity 85.1%; Pred. No. 4.5e-205;
Matches 1060; Conservative 0; Mismatches 185; Indels 0; Gaps 0;
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Db 988 TTTTACGGCAGGTGAAGAAATTTATGACCTTTTCTACATTTAAACATGTACTGTGAGCAATACT 1047
Qy 301 TTGAATTCATPCCAATTAAGCAATTTGGTACAGTTACTTTTACCAATTTGCAATTTCAATTTGGT 360
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Qy 481 GTTGATCCAAAGTGCATATTTGTATGCTTCAGAGTTATGCAAGTCTCAATTAAGGTCAACA 540
Db 1228 GTCGATCCAAAGGAGTACTTAACTGATTCAGAGTTATACCAAGTCTTCAACCAAGGTGCA 1287
Qy 541 ACTCTTTTGTGGCAACCAATGTTGAAATGGTTTACACATCTGTACAAATGGGTTCTCC 600
Db 1288 ACTCTTTTGTGGCAACCAATGTTGAAATGGTTTACACATCTGTACAAATGGGTTCTCC 1347
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Db 1348 AACACTTATGGTGAATGTTCAATTTGACTGTTCAATTAATTCATGTTGTTGATTTACAAAGGA 1407
Qy 661 TTAATGATTTGGAATTAATCCGGTTTCACTGGAATTCATTTAGTTTACACTAAACCTTTGATACA 720
Db 1408 TTGAATGATTTGGAATTAATCCGGTTTCACTGGAATTCATTTAGTTTACACTAAACCTTTGATACA 1467
Qy 721 TCTAATGGAATTCAGATTAATTAATCAAAATGTACTGCTGCTGTTATCGTCAATTTATTTGAT 780
Db 1468 TCTAATGGAATTCAGATTAATTAATCAAAATGTACTGCTGCTGTTATCGTCAATTTATTTGAT 1527
Qy 781 GCTTATATTTCTGCTACAGATGTTAAACCAATATACTTTAGCATATACCAATGATTTATACT 840
Db 1528 GCTTATATTTCTGCTACAGATGTTAACTCGTACACCTTGTGATGCTATGATGATATACT 1587
Qy 841 TGTGCTGGCAGTCTGCTGCAAGTAAACCTTTTCACTTTTAAAGATGGAGTGGATACAGAA 900
Db 1588 TGTGCTGGTGTATTGTCGCAACGTCACCTTTTCACTTTAAGATGGAGTGGATACAGAA 1647
Qy 901 AGTATGCCGATCTAAGGTTATTTGTCATTTGTTGCTACCACTAGAACAGTTTACAGACAGT 960
Db 1648 AGTATGCCGATCTAAGGTTATTTGTTATTTGTTGCTACTTACCAAGAGTTTACAGACAGT 1707
Qy 961 ACCACTGCTGCTACTCTTTACCACTTCAATTCAGATGTTGATAAAACCAAAACAATCGAA 1020
Db 1708 ACTACCGCGTGACCACTTACCACTTCAATTCAGATGTTGATAAAACCAAAACAATCGAA 1767
Qy 1021 ATTTTGCACACCTATTCCAAACCACTTACCACTTCAATTCAGATGTTGTTGTTGTTGTTGTTCC 1080
Db 1768 ATTTTGCACACCTATTCCAAACCACTTACCACTTCAATTCAGATGTTGTTGTTGTTGTTGTTCC 1827
Qy 1081 TATCTGACTAAGACTGACCACTAATTTGGTGAACAGCTACTGTTATTTGTTGTTGTTGTTGTTCCATAT 1140
Db 1828 TACCTGACCAAACTGACCACTAATTTGGGAAACTGCTACTGTTATTTGTTGTTGTTGTTGTTCCATAT 1887
Qy 1141 CATACTACCACTGTTTACCACTGTAATGGAGAGAAACAACTACTACCACCACTCACTCGT 1200
Db 1888 CACACTACCACTGTTTACCACTGTAATGGAGAGAAACAACTACTACCACCACTCACTCGT 1947
Qy 1201 ACCAATCCACTGATTCAATTTGACACAGTGGTGGTGTACAAAGTTCCA 1245

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Db      1948 ACTAATCCCACTGACTCAATAGACACTGTTCATTGTACAAGTTCCA 1992
|||||
|| |||||
RESULT 4
US-10-245-802-11
; Sequence 11, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 3360
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-245-802-11

```

Query Match	76.1%	Score 947.4;	DB 15;	Length 3360;
Best Local Similarity	85.1%	Pred. NO. 9.2e-205;		
Matches 1059;	Conservative	0;	Mismatches 186;	Indels 0;
Gaps 0;				

Qy	1	AAGACAATCACTGCTGTTTTGATAGTATTTAAATTCATTAACCTGGTCCAAATGCTGCTAAAT	60
Db	52	AAGACAATCACTGCTGTTTTCAACAGATTTTAAATTCATTCAGCTGGTCTAAATGCTGCTACT	111
Qy	61	TATGCTTTCAAAGGCGCCAGGATACCCAACTTGGAAATGCTGTTTTGGGTGGTCTCTTAGAT	120
Db	112	TATTAATTTAAGGACCCGGAACCCCAACTTGGAAATGCTGTTTTGGGTGGTCTCTTAGAT	171
Qy	121	GGTACCAGTGCCAATCCAGGGGATACATTCACATTTGAATATGCCATGCTGTCTTTAAATPAT	180
Db	172	GGTACTAGTGCAACTCCGGGAGATACATTCACATTTGAATATGCCATGCTGTCTTTAAATTT	231
Qy	181	ACTACTTCACAAAATCTGTGTTGATTTAACTCGCGATGCTGTTAAATATGCTACTCTGTCAA	240
Db	232	ACTACTTCTCAAAATCTGTGTTGATTTGACTGCTCATGGTGTTAAATATGCTACTACTGTCAA	291
Qy	241	TTTTTAATCTGCTGAAGAAATTCACAACTTTTTCTACATTAACATGTACTGTGCAAGACGCT	300
Db	292	TTTCAGGCGAGTGAAGAATTTATGACCTTTTCTACATTAACATGTACTGTGAGCAATACT	351
Qy	301	TTGAAATCATCCATTAAGGCATTTGGTACAGTTACTTTTACAAATGTCATTCAAATGTTGGT	360
Db	352	TTGACTCCATCTATTAAAGGCTTTGGGTACTGTCACCTTACCATTGCCATTCAAATGATAGT	411
Qy	361	GGACACAGGTTCAATCAACTGATTTGGAGATTTCTAAATGTTTTTACTGCTGGTACCACATACA	420
Db	412	GGAACTGGTCTCTCTGTTGATTTGGAAGATTCCTAAATGTTTTTACTGCTGGTACTATACACA	471
Qy	421	GTCACTTTAATGATGGTGTATAAAGATATCTCAATTCGATGTTGAGTGTGAAAAGTCAACC	480
Db	472	GTTACATTTAATGATGGTGGCAAGAAATCTCTATTAAATGTTGATTTTGAAGAGGTCAAAAT	531
Qy	481	GTTGATCCAAAGTGCAATATTTGTAATGCTTCCAGAGTTATGCCAGTCTCCTCAATAAGGTACAA	540
Db	532	GTCGATCCAAAAGGGTACTTTAACTGATTTCCAGAGTTATACCAAGTCTCAACAAAGGTGCA	591
Qy	541	ACTCTTTTTTGGGACCAACAATGTGAAAATGTTTACACATCTGGTACCAATGGGGTTCCTCC	600
Db	592	ACTCTTTTTTGTGCACCAACAATGTCCAAATGTTTACACATCTGGTACCAATGGGATTCGCT	651
Qy	601	AGTAGTAAACGGTGAACGTTGCTATTGATGTGCTCAAAATATTCATATTTGGTATCAAAAAGGA	660
Db	652	AACACTTATGTTGATGTTTCAAAATGCACTGTTCAAAATATTCATGTTGGTATTCAAAAGGA	711

RESIT.T 5

```

RESULTS 5
US-10-245-802-9
; Sequence 9, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST STREPTOCOCCUS DISSEMINAT
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 1404
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-245-802-9

```

	Query Match	71.9%;	Score 895;	DB 15;	Length 1404;
	Best Local Similarity	83.2%;	Pred. No. 4.9e-193;		
	Matches 1031;	Conservative	0;	Mismatches 205;	Indels 3; Gaps 1;
Qy	7	ATCACTGGTGTGTTTGGATAGCTTTTAATTCATTAACCTTGCTGCCAAGTGCCTCAATATGCT	66		
Db	58	ATTACGGGTGTTTTCAATAGCTTTTGTTCGTTGCATGGACAAGAGCTGGTAAATTATGCT	117		
Qy	67	TTCAAGGGCCAGGATACCAACTTGGAATGCTGTTTTGGGGTGGCTCCTTAGATGGTACC	126		
Db	118	TATTAAGGCCCAATAGACCAACTTGGAATGCTGTTTTGGGGTGGCTCCTTAGATGGTACT	177		

127 AGTCCCAATCCAGGGATACATTGCAATGGAATGCAATGCTGCTGTTTAAATATCTACT 186
Db |||||||
178 AGTCAAAATCCAGGAGACATTCATTTGAATATGCAATGCTGCTGTTTAAATATCTACT 237
Qy |||||||
Db |||||||
187 TCACAAACATCTGTTGATTTAACTGCGGATGGTGTAAATATGCTACTTGTCAATTTAT 246
Qy |||||||
Db |||||||
238 GATCAAAACATCTGTTGATTTGACCTGCTGAAGGTGTAAATATGCTACTCATGTGCTTTAT 297
Qy |||||||
Db |||||||
247 TCTGGTGAAGATTCACAACTTTTCTACATTAACATGCTACTGTGAAGGCTTTGAA 306
Qy |||||||
Db |||||||
298 TCAGGTGAAGATTTACAAACATTTTCTCATTAATGATGCTGTGAAGCAATCTTTAA 357
Qy |||||||
Db |||||||
307 TCATCCATTAAGGCAATTTGGTACAGTTACTTTTACCAATGCAATCAATGTTGGTGA 366
Qy |||||||
Db |||||||
358 TCATCTATTAAAGCTTTGGGTACCGTTACTTTTCAATTTCAATTTTAAATGTTGGTGA 417
Qy |||||||
Db |||||||
367 GGTTCATCAATGATTTGGTGAAGATTTCTAAATGTTTAACTGCTGTGATCAATPACAGTCA 426
Qy |||||||
Db |||||||
418 GGTTCATCGTTGATTTGGTGAAGTTCCTCAATGTTTAAAGGCTGCGCACCACACAGTTACT 477
Qy |||||||
Db |||||||
427 TTTAATGATGATTAAGATATCTCAATGATGTTGAGTTTGAAGTCAACCGTTGAT 486
Qy |||||||
Db |||||||
478 TTTAATGATGATTAAGATATCTCAATGATGTTGAGTTTGAAGTCAACCGTTGAT 537
Qy |||||||
Db |||||||
487 CCAAGTGCATATTTGTATGCTTCCAGAGTTATGCCAGTCTCAATTAAGTTCACAACTCTT 546
Qy |||||||
Db |||||||
538 GCAAGTGTGATTTTCAATAGCTCAAGCTTATCCAGTATTAACAAGATTTCAATCACT 597
Qy |||||||
Db |||||||
547 TTTGTGACCAACATGTAAGATTTGTTTACATCTGATCAATGCGGTCTCCAGTAGT 606
Qy |||||||
Db |||||||
598 TATGTGGACCAACATGTAAGATTTGTTTACATCTGATCAATGCGGTCTCCAGTAGT 657
Qy |||||||
Db |||||||
607 AACGCTGATGTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 666
Qy |||||||
Db |||||||
658 ACTGTGACACTACTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 717
Qy |||||||
Db |||||||
667 GATTTGGAATATCCGGTTTCACTGAAATCATTTAGTTACACTTAAATGTTGATCACTAAT 726
Qy |||||||
Db |||||||
718 GATTTGGAATATCCGGTTTCACTGAAATCATTTAGTTACACTTAAATGTTGATCACTAAT 777
Qy |||||||
Db |||||||
727 GGAATTCAGATTAATCAAAATGATCTGCTGTTTATCGTCCATTTATTTGATGCTTAT 786
Qy |||||||
Db |||||||
778 GGTATTTCTATCACAATGAAATGTCCTGCTGTTTATCGTCCATTTATTTGATGCTTAT 837
Qy |||||||
Db |||||||
787 ATTCTGCTACAGATTTAAACAATATCTTTAGCATATACCAATGATTTACTTGTCT 846
Qy |||||||
Db |||||||
838 ACTCTGCTGCTGAGGCGCAAGACAGACA---ATTAGATATATCTAATGATTTATGCTGTT 894
Qy |||||||
Db |||||||
847 GGCAGTCTGCTGCAAGTAAACCTTTCACTTTTATGATGCTGATACCAAGATAGTAT 906
Qy |||||||
Db |||||||
895 GGTAGTTCCTTACAAAGTAAAGCGGTTCATTTTAAAGTTGAGAGGATACCAATTAAGTGA 954
Qy |||||||
Db |||||||
907 GCGGATCTAAGCGTATTTGATTTGCTGCTCAAACTAGAACAGTTTACAGACAGTACCACT 966
Qy |||||||
Db |||||||
955 GCTAATTTCTAAGCGTTTGTCTATTTGCTACCAACCGGACAGTTTACTGACAGTACTACT 1014
Qy |||||||
Db |||||||
967 GCTGTCTACTTTTACCAATCAATCCAAAGTGTGATTAACCAAAACCAATGAAATTTTG 1026
Qy |||||||
Db |||||||
1015 GCTGTCTACTTTTACCAATCAATCCAAAGTGTGATTAACCAAAACCAATGAAATTTTG 1074
Qy |||||||
Db |||||||
1027 CAACCTATTCNAACCACTACCAATCAATCTTATGTTGTTGATGCTACTTCTTATCTG 1086
Qy |||||||
Db |||||||
1075 CAACCTATTCNAACCACTACCAATCAATCTTATGTTGTTGATGCTACTTCTTATCTG 1134
Qy |||||||
Db |||||||
1087 ACTAAGATGCAACCAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1146
Qy |||||||
Db |||||||
1135 ACTAAGATGCAACCAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1194
Qy |||||||
Db |||||||
1147 ACCCAACTGTTTACAGTGAATGGACAGGAAACAACTACTACCAACCAACTGCTACCAAT 1206
Qy |||||||
Db |||||||
1195 ACCCAACTGTTTACAGTGAATGGACAGGAAACAACTACTACCAACCAACTGCTACCAAT 1254
Qy |||||||
Db |||||||

Qy 1207 CCAACTGATTTCAATTTGACACAGTGGTGGTACAAAGTTCCA 1245
Db |||||||
1255 CCAACTGATTTCTATAGATACTGTCGTTGTGCAAGTTCCA 1293
Db |||||||

RESULT 6

US-10-245-802-13
; Sequence 13, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 1407
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-245-802-13

Query Match 58.9%; Score 733.4; DB 15; Length 1407;
Best Local Similarity 74.5%; Pred. No. 2.6e-156;
Matches 923; Conservative 0; Mismatches 316; Indels 0; Gaps 0;

Qy 7 ATCACTCGTGTGTTTGTATAGTTTAAATTCATTAACTTGGTCCAAATGCTGCTTAATATGCT 66
Db |||||||
58 ATTACAGTGTGTTTCAATAGTTTAAATTCGTTAACTTGGGCCAATGCTGCTTCTTATCCA 117
Qy 67 TTCAAAGGCCAGGATACCCAACTTGAATGCTGTTTGGGTGGTCTTAGATGGTACC 126
Db |||||||
118 TATAGAGTCCAGCTACTCTCTACTTGGACCGCTTAATAGATGGTCTTTAGATGGAGCT 177
Qy 127 AGTGCCCAATCCAGGGGATACATTCAATTTGAATATGCAATGCTGCTGTTTAAATATATACTACT 186
Db |||||||
178 ACTGCTAGTGTGTTGATGACATTCACGTTAGACATGCTGTTGTTTCAATTTATTA 237
Qy 187 TCACAAACATCTGTTGATTTTAACTGCGGATGGTGTAAATATGCTACTTGTCAATTTTAT 246
Db |||||||
238 GATCAAAGCTCAATTTGATTTAGTTGCTGATGGTCTACTTATGCTACTTGTAAATTTGAAT 297
Qy 247 TCTGGTGAAGATTTCAACATTTTCTTACATTAACATGCTACTGTGAAGCGCTTTGAA 306
Db |||||||
298 TCTGCCGAAGAGTTTACTACTTTTCTAGTGTGCTACTGTGCTACTTACCAATGACT 357
Qy 307 TCATCCATTAAGGCATTTGGTACAGTTTACTTTTACCAATGCTCAATTTGTTGGTGAACA 366
Db |||||||
358 GCTGACACCAAGCCATAGGAACCTGTAACTTACTTCTCTTCTCAGTGTGGGGGATCA 417
Qy 367 GGTTCATCAACTGATTTTGGAGATTTCTAAATGTTTATCTGCTGTGATCAATPACAGTCA 426
Db |||||||
418 GGTTCAGATGTTGATTTGGCAAAATTCCTCAATGTTTACTCTGCGAGGAATCAATACAGTTACT 477
Qy 427 TTTAATGATGATTAAGATATCTCAATGATGTTGAGTTTGAAGTCAACCGTTGAT 486
Db |||||||
478 TTTAATGATGATTAAGATATCTCAATGATGTTGAGTTTGAAGTCAACCGTTGAT 537
Qy 487 CCAAGTGCATATTTGTATGCTTCCAGAGTTATGCCAGTCTCAATTAAGGTCAACACTCTT 546
Db |||||||
538 TCCAGCGCATCTGATCTTGTGTTCAAGAAATTTTACCGAGTCTTTCACAGCAGTAAATCTT 597
Qy 547 TTTGTGGCACAACATGTTGAATGTTTGAATGTTTGAATGTTTGAATGTTTGAATGTTTGA 606
Db |||||||
598 TTTCTTCCCCAAGAAATGTGCAAAATGGTTTATCTTCTGTTGATCAATGGGATTTTCGACTGCT 657
Qy 607 AACGGTGAAGTGTGCTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 666
Db |||||||
658 GGTACTGCTGCTACTATAGATTTGTTTCCAAGTTCATGTCGGGATATCAAAATGGGTTGAAT 717
Db |||||||

Db 115 GCTCGATACGAAGAAATATCTACTCTTACCGCTAAATGCTCAATGGAAATGGGCTTTGGAT 174
Qy 121 GGTACACAGTCCCAATCCAGGGGTACATTCACATTTGAATATGCAATGCTGTTGTTAAATAT 180
Db 175 GGTACTATTGCCAGTCCCGGTGATACAAATTTACATTTAGTCATGCGCCTGTGTATATAAATC 234
Qy 181 ACTACTTTCACAAACATCTGTGTGTTTAACTGCCGATGGTGTAAATATGCTACTTTGTCAA 240
Db 235 ATGACGTACGAAACCTCAGTGCATTAATCTGCACTCTATTCATATGATGCACATGTGAC 294
Qy 241 TTTTATTTCTGGTGAAGAAATTCACAACTTTTTCATATTAACATGCTGTGGAACGAGCT 300
Db 295 TTTGATGCTGTGGAAGACACTAAAGTTTTCAGATTTGAAGTGTACGGTGCATGTGAG 354
Qy 301 TTGAAATCATCCATTAGGCAATTTGGTGTACAGTTACTTTTACCAATGTCATTCATTTGGT 360
Db 355 TTGACAGAAGATACCAGCGTTTTTGGAAAGTGTATTTTGGCTATTTGCTTTTCAATGTTGGA 414
Qy 361 GGACACAGTTTCATCAACTGATTTTGGAAAGATTTCTAAATGTTTACTGCTGTGTACCAATACA 420
Db 415 GTTTCGGATCTAAATCTACGATTAACAGACTCCAAATGTTTTCAGTGGGTACACACT 474
Qy 421 GTCACTTTTAAATGATGTGATAAAGATATCTCAATGATGTTGAGTTTGAAGTCAACC 480
Db 475 GTCAAGTTTTTGGACGGAACAATCAACTTCTACAACTGCAAAATTTTCTTCCCGGAAGA 534
Qy 481 GTTGATCCAAGTGCATATTTGTATGCTTCAGAGTTATGCAAGTCTCAATAGGTGACA 540
Db 535 GAACTAGCGTTTGGTCTAGTTGTTAGTCAAGACTTTCCATGTGCTGCGATACAATGACT 594
Qy 541 ACTCTTTTGTGGCACCACCAATGTGAAATGGTTTACACATCTGCTGCAATGGGGTCTCC 600
Db 595 AATTTTGTATGCTACACCTGTTTTCATGGTTATCAGCTGGGTAGTTAGTTTACA 654
Qy 601 AGTAGTAACCGTGCAGTTGCTATTGATGTCTCAAAATATCATATGTTGTATCAAAAGGA 660
Db 655 TCTAATGATGATGATTTTGAATTTGATGTTCTTCTATACATGTTGTGATAAATCAATGAA 714
Qy 661 TTAATCATTTGGAATATCCGGTTTTCATCTGMAATCTTAGTTAGTACATTAACCTGTGACA 720
Db 715 ATAATGATTTGAGTATGCCAGTATCTCTGTTCCCTTCGATCATATCTAAGATGACA 774
Qy 721 TCTAATGGAATTCAGATTAATATCAAAATGTACTGCTGGTTATCTGCTCCATTTATGAT 780
Db 775 TCAGTGCACCTTTACATTTAGTTTAAACAATCTCTCGAGTTATCGACCTTTTGTGAT 834
Qy 781 GCTTATATTTCTGCTACAGATGTTTAAACAATATATCTTTAGCATATACCAATGATATACT 840
Db 835 GCGATTGTTCAAATACCAACGACAGAACCTTTTGTGTAATAATATACCAATGAGTTTGC 894
Qy 841 TGTCTGGCAGTCTGTGCAAGTAAACCTTTTAC ---TTTAAAGATGAGTGGATACAAG 897
Db 895 TGTGTGAATGTCATATACAGTCCATACCTTTTCAAGTTTCTTTTCTCAGCCCAATTTTA 954
Qy 898 AATAGTATGTCGGATCTAACCGTATTTGTCATTTGCTGCTACCACTAGAACAGTTTACAGAC 957
Db 955 TATCAGCAGGCTTTAGCTATTGTTGGTGCAGACTAGTTGTTACCATCCACAGTATAGTT 1014
Qy 958 AGTACCACTGCTGCTACATCTTTTACCAATTCATCCAAAGTGTGTGATAAAACCAAAATC 1017
Db 1015 TCCATTACCAAGATACCAATTAACCTTTCAATTTCCCGACTCCAGAAAACCAAAACAATT 1074
Qy 1018 GAAATTTTGCACCTATTCCAAACCACTACCATCAACCTTCATATGTTGGTGTGACTACT 1077
Db 1075 CTAGTCTTAGAGCCCATACCCACACTACGGTAAACAATTCACACCAATGGCTTTGATACT 1134
Qy 1078 TCCTATCTGATAAGACTGCAACCAATTTGGTGAACAGCTACTGTTATTTGTTGATGTGCCA 1137
Db 1135 TGGTATATATCTAAGAAAGCCACCATTTGGTGCACAGCTACTGTTTTCATTGATGTTCCA 1194
Qy 1138 TATCATACTACCAACTGTTTACAGTGAATGGACAGGAACATTCATCACCAACCAACT 1197

Db 1195 CAACATACAGCTACTTTTGTACCATATATGCGCAAGATCAAGTACGCGCAACCACT 1254
Qy 1198 CGTACCACATCCCACTGATTCATTTGACACAGTGGTGGTACAAAGTTCCA 1245
Db 1255 TACTTCGATGACATAGACTTGGTGTGATCTGTGTCATTTGTGAAATTTCCA 1302
RESULT 10
US-09-864-761-2885
; Sequence 2885, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 2885
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000018.2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1

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; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.4
US-09-864-761-2885

Query Match      4.4%   Score 55.4; DB 9; Length 436;
Best Local Similarity 48.6%; Pred. No. 0.019;
Matches 152; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

QY 914 CTAACGGTATTGTCATTGTTGCTACACTAGAACAGTTACAGACAGTACCACCTGCTGTCA 973
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 68 CTATTGTCACACTACTATTACCACCTACCACTAGTACTACCACCACCTATCATCACTACCATCA 127

QY 974 CTACTTTACCAATCAATCCAAAGCTTGTATTAACCAAAACAATCGAAATTTTGCACCTA 1033
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 128 CTACTAATATCTATCATTTACCACCTACTATTACCACTTACCACGCACTATCATTTACTACTA 187

QY 1034 TTCCACCACTACCAATCACTACCAACTTTTCATATGTTGGTGTGACTTCTTCTATCTGACTAAGA 1093
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 188 CCACCTCCACATTTACTACTACTAATGCTATCATTTACTACTGCTTCTATTAATTTACTA 247

QY 1094 CTGCACCAATTTGGTGAACAGCTACTGTTATTGTTGATGTGCCATATCATACTACCAAA 1153
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 248 CTCCTACTCTTACCATTACTACTACTAGTAGTAGTATCACCACTTACTACTATCATTA 307

QY 1154 CTGTTACAGTGAATGGACAGGAAACATCACTACACACAACTCGTACCAATCACTG 1213
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 308 CTATTACCACCACTACTACTACTATCATTTACTACTTACCACCACCACTACTACTACTG 367

QY 1214 ATTCAATTGACAC 1226
      ||| ||| |||
DB 368 CTGTCATTACTAC 380

RESULT 11
US-10-282-122A-27975/c
; Sequence 27975, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308

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Db 6240 CCAACTACCCCTCTACTACACCAATACTTCAACTACCCCTCTACTACACCAATACT 6181
QY 919 GGTATTGTCATTGTTGCTACAACTAGAACAGTTTACAGACAGTACCACTGCTGCTACTACT 978
Db 6180 TCAACTACCCCTCTCTCTCTCCAAATCTTTAACTACCCCTACTACTCTCTAACTACT 6121
QY 979 TTACCATTCATCCAACTGTTGATATAAACCMAAACAATCGAAATTTTGGCAACTATTCCA 1038
Db 6120 TCAACTACAAACACCTACTACTCTTAAACCCCACTACTACCCCTTCTTAATATCTCCAAATACT 6061
QY 1039 ACAGTACCATCAAACTTCTATATGTTGGTGTGACTACTTCCCTATCTGACTAGACTGCA 1098
Db 6060 CCAACTACCCCTCTCTACTACTTCCAAATCTTCAACTACCCCTCTCTCTCCAACTACT 6001
QY 1099 CCAATTGGTGAACAGCTACTGTTTATTGTTGATGTGCGCATATCATATACCAAACTGTT 1158
Db 6000 CCAATTACCCCTCTACTACTTCCAAATCTTAACTACCCCTCTCTACTTCCAAATACT 5941
QY 1159 ACCAGTGA---ATGACAGGAACAATCACTACCAACCAAACTCGTACCAATCCAACTGAT 1215
Db 5940 TCAACTACCCCATCTACTACTCTTAAACCTCTAACTACTTCTCTCTACTAATCCAAATACT 5881
QY 1216 TCAATTGACAC 1226
Db 5880 TCAACTACCCCT 5870

RESULT 13
US-09-968-007A-427
; Sequence 427, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa
; FILE REFERENCE: 689290-71
; CURRENT APPLICATION NUMBER: US/09/968,007A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,172
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,173
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,278
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,294
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,295
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,316
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 1001
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 427
; LENGTH: 267156
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-007A-427

Query Match 3.9%; Score 48.8; DB 11; Length 267156;
Best Local Similarity 46.2%; Pred. No. 14;
Matches 241; Conservative 0; Mismatches 272; Indels 9; Gaps 2;

QY 704 ACACATAAACTTGATCACTTAATGGAATTCAGATTAAATATCAAAATGTACTGCTGGTT 763
Db 12574 ATACTACCACTGGCACTACTGATGATGTTCTATACACCAATCTTTCCCAAGTACTA 12633
QY 764 ATCGTCCATTTATTGATGCTTATATTTCTGCTACAGATGTTAAACATATATCTTTAGCAT 823
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QY 824 ATACCAATGATTATCTTGCTGGCAGTGTCTGCAAGTAAACCTTTTCACTTTTAGAT 883
Db 12691 CTACTAATGCTAGCACTAATGCTACTGTTCTCTCTACAAACCAACCTTTTCCCAACAAGTA 12750

QY 884 GGACTCGATACAGAATACTGATGCGGATCTTAACGGTATTGTCATTGTTGCTACAACTA 943
Db 12751 CTATTGGTGTTAACAATAATGCTACTGTTTCCCAATAACAACCTGCTTTTCCCAACAAATG 12810
QY 944 GAACAGTTACAGACAGTACCACTGCTG-----TCACTACTTTTACCATTCAATCCAAAGT 997
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QY 998 TTGATAAAACCAAAACAATCGAAATTTTGCACCACTATTCCAAACCACTACCATCACAACCTT 1057
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QY 1118 CTGTTATTCTTGTGTCATATCATCTACCACTGTTTACCAGTGAATGACAGGAA 1177
Db 12991 CTATTAGTGTTAACAATACTAGTACTGTTTCTGTGATACAACTGCTCTTTCCCTTACAAGTA 13050
QY 1178 CAATCACTACCAACCAACTCGTACCAATCCAACTGATTCAA 1219
Db 13051 CTACTAGTCTAGCACTAATGCTACCCCTGTTCTTATCACA 13092

RESULT 14
US-09-263-959-1
; Sequence 1, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy B.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 684973 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-1

Query Match 3.9%; Score 48.8; DB 9; Length 684973;
Best Local Similarity 46.2%; Pred. No. 23;
Matches 241; Conservative 0; Mismatches 272; Indels 9; Gaps 2;

QY 704 ACACATAAACTTGATCACTTAATGGAATTCAGATTAAATATCAAAATGTACTGCTGGTT 763

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Qy 884 GGACTGGATACAAGATAGTATGCGGATCTAAACGGTATTTGTCATTTGCTGCTACAAGTA 943
Db 12751 CTATTTGGTGTACAACTAATGCTACTGTTCTCCCAATACAACTGCGCCCTTTTCCCAACAAAGT 12810
Qy 944 GAACAGTTTACAGAGTACCACTGCTG-----TCACTACTTTTACCATTCAATCCAAGTG 997
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Qy 998 TTGATAAAACCAAAACCAATCGAAATTTTGGCAACCTATTTCCAACCACTACCAATCACAACCTT 1057
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Qy 1118 CTGTTATTTGGTGTGCGCATATCATCTACTATCTATCTGCTAGTAAAGTGCACCAATTTGGTGAACAGCTA 1177
Db 12991 CTATTTAGTGTACAACTAGTACTACTGTTCTGATACAACTGCTCTCTTTCCCTACAAGTA 13050
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Db 13051 CTACTAGTGTAGCACTAATGCTACCCCTGTTCTTATCACA 13092

RESULT 15
US-10-282-122A-16859/c
; Sequence 16859, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA 034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16859
; LENGTH: 1893
; TYPE: DNA
; ORGANISM: Clostridium difficile
; US-10-282-122A-16859

Query Match 3.8%; Score 47; DB 17; Length 1893;
Best Local Similarity 42.3%; Pred. No. 3.1;
Matches 257; Conservative 0; Mismatches 350; Indels 0; Gaps 0;
Qy 144 TACATTCACATTTGAATATGCGATGTTGTTAAATATGCTACTTGTCAATTTTATTTCTGGTGAAGAATTCAC 203
Db 1509 TCCACCACACTATTCTTAATTTCTTTTCTTTTAAATAATTTTTCAGCATTTTCGATCTAATTC 1450
Qy 204 TTTAACTGCGAGTGGTGTAAATATGCTACTTGTCAATTTTATTTCTGGTGAAGAATTCAC 263
Db 1449 GTTACCTGTAACTATTATTGGAGCACCATAATGAGAGCTCTAGCTGATATATCTCATAGC 1390
Qy 264 AACTTTTCTACATTAACATGTACTGTGAACGAGCGCTTTGAAATTCATCCATTAAGGCAAT 323
Db 1389 ATCAGCTTCTCCATTTCCACCTACTACAAAAGCAGTCTTAAATGTAATCTTTTAAATCTTT 1330
Qy 324 TGGTACAGTGTACTTTTACCAATGTCATTCATGTTGGTGGAAACAGGTTTCATCAACTGATTT 383
Db 1329 TGTATTCTTAAAGAAAGTTTCAAAATCTATCTTCTCCAGAAAACCTCTCTCAACTTTTACTTAC 1270
Qy 384 GGAAGATTTCAATGTTTACTGCTGATCAATACAGTACAGTACATTTTAAATGATGCTGATAA 443
Db 1269 ACCTAATTTAGAAAGTTTCTTTCAGTTTCTTTTGATATCTTTAGATTTCTCCACCTACTAT 1210
Qy 444 AGATATCTCAATTTGATGTTGAGTTTGAAGAGTCAACCGTTGATCCAAAGTGCATATTTGTA 503
Db 1209 ATATATTTTCTTAGAAGATAGATTTACTTCCAGTACTCTTAAATATTTTTCAGCTTCTATTTTC 1150
Qy 504 TGTCTCCAGAGTTATGCGCAAGTCTCAATAAGGTCAACAATCTTTTGTGGGACCAACAATG 563
Db 1149 TGATGGTAGTGAATCTTTTGTAGATAATAATATTGGTGCATTTTGTGGAGGCAAGTGG 1090
Qy 564 TGAATATGGTTACATCTGCTACAAATGGGGTCTCCAGTAGTAACCGTGCAGCTTGTCTAT 623
Db 1089 TGTGATGCTAATCCCACTATAGCATCTTCTCCAACTAAAATTTATAGCTTCTGCTTC 1030
Qy 624 TGATTGCTCAAAATATTCATATTGGTATCACAAGAGGATTAATGATTGGAAATTTATCCGGT 683
Db 1029 TCCATCTTTGAATCTCTTTTACTTAATCTTCTGCTGTTGTAATCTTGAATCACCAGA 970
Qy 684 TTCATCTGAATCAATTTAGTTTACATAAACTTGTACATCTTAATGGAATTCAGATTAATA 743
Db 969 TAAACCTCTACTTTTAAATTTCTTTTCCATCTTTTACATCAGTTAATTAATCTTTGTGTAAGTC 910
Qy 744 TCAAAAT 750
Db 909 TCTAACT 903

Search completed: March 24, 2005, 07:52:14
Job time : 1818 secs

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OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 09:36:50 ; Search time 179 Seconds
(without alignments)

11380.807 Million cell updates/sec

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1225.8	98.5	3573	4	US-09-248-796A-2140 Sequence 2140, Ap
2	1029	82.7	2340	4	US-09-248-796A-2599 Sequence 2599, Ap
3	728.2	58.5	1536	4	US-09-248-796A-22 Sequence 22, Appl
4	671.6	53.9	3180	4	US-09-248-796A-20 Sequence 20, Appl
5	574.6	46.2	1941	4	US-09-248-796A-2598 Sequence 2598, Ap
6	509.8	40.9	900	4	US-09-248-796A-2142 Sequence 2142, Ap
7	414.6	33.3	690	4	US-09-248-796A-2595 Sequence 2595, Ap
8	392	31.5	2436	4	US-09-248-796A-2141 Sequence 2141, Ap
9	293.2	23.6	699	4	US-09-248-796A-19 Sequence 19, Appl
10	253.6	20.4	462	4	US-09-248-796A-16 Sequence 16, Appl
11	149.8	12.0	294	4	US-09-248-796A-9483 Sequence 9483, Ap
12	82.4	6.6	100	1	US-08-145-705A-32 Sequence 32, Appl
13	82.4	6.6	100	1	US-08-145-705A-34 Sequence 34, Appl
14	76	6.1	100	1	US-08-145-705A-33 Sequence 33, Appl
15	68	5.5	100	1	US-08-145-705A-36 Sequence 36, Appl
16	61.4	4.9	5511	3	US-08-928-361B-2 Sequence 2, Appli
17	61.4	4.9	5511	4	US-09-588-995A-2 Sequence 1, Appli
18	61.4	4.9	7334	3	US-08-928-361B-1 Sequence 1, Appli
19	61.4	4.9	7334	4	US-09-588-995A-1 Sequence 37, Appl
20	57.2	4.6	100	1	US-08-145-705A-37 Sequence 35, Appl
21	57	4.6	100	1	US-08-145-705A-35 Sequence 180704, A
22	55.4	4.4	601	4	US-09-949-016-180704 Sequence 16938, A
23	55.4	4.4	70770	4	US-08-700-651-1 Sequence 1, Appli
24	55.2	4.4	5163	3	US-08-928-361B-4 Sequence 4, Appli
25	55.2	4.4	5163	4	US-09-588-995A-4 Sequence 4, Appli
26	55.2	4.4	5318	3	US-08-700-651-2 Sequence 2, Appli
27	55.2	4.4	5318	3	US-08-700-651-2 Sequence 2, Appli

28	55.2	4.4	5318	3	US-08-928-361B-3 Sequence 3, Appli
29	55.2	4.4	5318	4	US-09-588-995A-3 Sequence 3, Appli
30	53.6	4.3	528	4	US-09-248-796A-2593 Sequence 2593, Ap
31	53.6	4.3	832	4	US-09-621-976-2813 Sequence 2813, Ap
32	52.8	4.2	1506	4	US-09-248-796A-15 Sequence 15, Appl
33	51.2	4.1	1141	4	US-09-806-708B-22 Sequence 22, Appl
34	50.6	4.1	1671	4	US-09-248-796A-8235 Sequence 8235, Ap
35	50	4.0	1071	1	US-08-357-962-1 Sequence 1, Appli
36	50	4.0	1071	1	US-08-878-106-1 Sequence 1, Appli
37	49.2	4.0	832	1	US-09-621-976-2813 Sequence 5, Appli
38	48.6	3.9	425	1	US-08-357-962-5 Sequence 5, Appli
39	48.6	3.9	425	1	US-08-878-106-5 Sequence 22, Appl
40	48.6	3.9	1141	4	US-09-806-708B-22 Sequence 13610, A
41	47.6	3.8	83428	4	US-09-949-016-13610 Sequence 23, Appl
42	47	3.8	1158	4	US-09-248-796A-23 Sequence 18, Appl
43	47	3.8	1569	4	US-09-248-796A-18 Sequence 4495, Ap
44	46.6	3.7	4184	4	US-09-949-016-4495 Sequence 16237, A
45	46.6	3.7	12191	4	US-09-949-016-16237 Sequence 16237, A

ALIGNMENTS

RESULT 1

US-09-248-796A-2140
; Sequence 2140, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Kelch Weinstein et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBIC

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 2140

; LENGTH: 3573

; TYPE: DNA

; ORGANISM: Candida albicans

US-09-248-796A-2140

Query Match 98.5%; Score 1225.8; DB 4; Length 3573;
Best Local Similarity 99.0%; Pred. No. 6.8e-313; Indels 0; Gaps 0;
Matches 1233; Conservative 0; Mismatches 12;

Qy	1	AAGACAATCACTGCTGTTTTTGATGATGTTTTTAATTCATTAACTTGGTCCAATGCTGCTAAT	60
Db	58	AAGACAATCACTGCTGTTTTTGATGATGTTTTTAATTCATTAACTTGGTCCAATGCTGCTAAT	117
Qy	61	TATGCTTTCAAAGGGCCAGGATACCCAACTTGGAAATGCTGTTTTGGGTGCTCTAGAT	120
Db	118	TATGCTTTCAAAGGGCCAGGATACCCAACTTGGAAATGCTGTTTTGGGTGCTCTAGAT	177
Qy	121	GGTACCACTGCCATCCAGGGGATACATTCATGATATGCCATGCTGTTTAAATAT	180
Db	178	GGTACCACTGCCATCCAGGGGATACATTCATGATATGCCATGCTGTTTAAATAT	237
Qy	181	ACTACTTCACAAAACATCTGTTGATTTAACTCCGATGGTGTAAATATGCTACTTGTCAA	240
Db	238	ACTACTTCACAAAACATCTGTTGATTTAACTCCGATGGTGTAAATATGCTACTTGTCAA	297
Qy	241	TTTTATTCTGCTGAAGAAATTCACAACTTTTCTCATTTAAACATGCTGTGAACACGCT	300
Db	298	TTTTATTCTGCTGAAGAAATTCACAACTTTTCTCATTTAAACATGCTGTGAACACGCT	357
Qy	301	TTGAATCATCCATTAAAGGCATTTGGTACAGTACTTTTACCAATTCGATTCGAATGCTGT	360
Db	358	TTGAATCATCCATTAAAGGCATTTGGTACAGTACTTTTACCAATTCGATTCGAATGCTGT	417

Qy	841	TGTCGTGCGAGTCGTCTGCGAAGTAACCTTTTCACTTTAAGATGCGACTGGATACAGAAT	900
Db	898	TTTCTGTGATGATTAATTGGCAACATGCACTTTTCACTTTAAGATGCGACTGGATATAAGAAT	957
Qy	901	AGTCATGCGCGGATCTTAACGGTATGTGCATTTGTCTCAACTAGAACAGTTTACAGACAGT	960
Db	958	AGTGATGCGCGGATCTTAACGGTATTTGTCAATGTTGCTCACTAGAACAGTTTACAGACAGT	1017
Qy	961	ACCACTGCTGTCACTACTTTTACCATTTCAAATCCAAAGTGTGTATAAAACCAAAACAATCGAA	1020
Db	1018	ACCACTGCTGTGTCAGTACTTTTACCATTTCAAATCCAAAGTGTGTATAAAACCAAAACAATCGAA	1077
Qy	1021	ATTTTGCAAACCTATTTCCAACCACTACCACTTCCATTAATGTTGGTGTGACTACTTCC	1080
Db	1078	ATTTTGCAAACCTATTTCCAACCACTACCACTTCCATTAATGTTGGTGTGACTACTTCC	1137
Qy	1081	TATCTGACTATAGACTGCGACCAATTTGGTGAACAGCTACTGTTATTTGTGATGCCCATAT	1140
Db	1138	TATCTGACTATAGACTGCGACCAATTTGGTGAACAGCTACTGTTATTTGTGATGCCCATAT	1197
Qy	1141	CATACTACCAACCTGTTTACCAGTGAATGCGACAGGAAACAATCACTACCAACCAACTCGT	1200
Db	1198	CATACTACCAACCTGTTTACCAGTGAATGCGACAGGAAACAATCACTACCAACCAACTCGT	1257
Qy	1201	ACCAATCCAACTGATTTCAATTTGACACAGTGTGGTACAAGTTCCA	1245
Db	1258	ACCAATCCAAATGATTTCAATTTGACACAGTGTGGTACAAGTTCCA	1302

RESULT 3

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US-09-248-796A-22
; Sequence 22, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 22
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-22

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Query Match	58.5%	Score	728.2	DB 4	Length	1536			
Best Local Similarity	74.1%	Pred. No.	6.5e-182						
Matches	922	Conservative	0	Mismatches	323	Indels	0	Gaps	0
Qy	1	AAGACAATCACTGCTGTTTTTGATAGTTTTTAATTCATTAACTTGTGTCCAAATGCTGCTAAT	60						
Db	76	AAGGTTATACGGGCAATTTTCGATAGTTTTTAATTCGTTAACTTGGACCAATGCTGCTCT	135						
Qy	61	TATGCTTTCAAAGGCCGAGATACCAACTTGGATGCTGTTTTGGTGTGCTCTAGAT	120						
Db	136	TATTCAATATAGAGTCCAGCTTAATCCTACTTGGACCGCTGAATAGGATGGTCTTTAGT	195						
Qy	121	GGTACCAAGTGCCAATCCAGGGGATACATTCATTCGATATGCCATGTGTGTTTAAATAT	180						
Db	196	GGAGCTACTGCTAGTGTGCTGTGACACATTCACGTTAGACATGCCATGTGTTTCAAAATTT	255						
Qy	181	ACTACTTCAAAAATCTGTGTTGATTTAACTCCGATGCTGTTAAATATGCTACTTGTCAA	240						
Db	256	ATTACTGATCAAAAGTCAATTTGATTTAGTGTGATGGTCGTACTTATGTCTACTTTGTAAT	315						
Qy	241	TTTTTATTCGTGTGAAGAAATTCACAACTTTTTTCTACATTAAACATGTACTGTGAACGACGCT	300						

Db	316	TTGAATCTGCGCGAAGAGTTTACTACTTTTCTAGTGTGCTCAAGTACTGTGACTACTACA	375
Qy	301	TTGAAATCATCCATTAAAGGCAATTGGTGACAGTTTACTTTTACCAAATTGCATTCAATGTTGGT	360
Db	376	ATGACTGCTGACACCAAGCCATAGGNACTGTAA CATTACCTTTCTCTATTCACTGTGGG	435
Qy	361	GGAAACAGGTTCACTCACTGATTTGGAGAGTTCTTAATGTTTTTACTGCTGTGACCAATACA	420
Db	436	GGATCAGGTTTCAGATGTTGATTTGGCAAAATTTCTCAATGTTTACTGCGAGGAATCAATACA	495
Qy	421	GTCACATTTAAATGATGGTGATAAAGATATCTCAAATTTGATTTGAGTTTGGAAAGTCAACC	480
Db	496	GTTTACTTTTAATGATGGTGACACTAGCAATTCGGCAACAGTTTGATTTTGAAAAATCAACC	555
Qy	481	GTTTGATCCAAAGTGCAATTTGTATGTTTCCAGAGTTATGCCAAGTCTCAATTAAGTGCACA	540
Db	556	GTGGCCTCCAGCGATCGTATCTTGTGTCAAGAAATTTTACCAGTCTTTTCACARGCGTA	615
Qy	541	ACTCTTTTGTGSCACCAATGTTGAAAATGGTTACACATCTGGTGACAAATGGGTTCTCC	600
Db	616	AGTCTTTTCTTCCCAAGAAATGTCNAATGGTTATCTTCTGTGTACAAATGGGATTTTCA	675
Qy	601	AGTAGTAAACGGTGACGTTGCTATTTGATGCTCAAAATATTCATATTTGGTATACAAAGA	660
Db	676	ACTGCTGGTACTGGTGCTACTATAGATTTGTCCACAGTTTCATGTCGGGATATCAAAATGG	735
Qy	661	TTAAATGATTTGGAAATTTATCGGGTTTCATCTGAAATCAATTTAGTTTACACTAAAATCTGTACA	720
Db	736	TTGAATGATTTGGAAATTTATCCAAATTTCACTGGGAATCTTTTCTTACAAANGACCTGTACA	795
Qy	721	TCTAAATGGAAATCAGAAATTAATAATCAAAATGTACCTGCTGGTATTGCGTCCATTATTTGAT	780
Db	796	TCAACAGTGTTTTAGTAACTATCAGAAATGTTCTCGCCGGATATCGTCCATTTGTCGAT	855
Qy	781	GCTTATATTTCTGCTACAGATGTTAAACCAATATATCTTTAGCATATACCAATGATATACT	840
Db	856	GCTTATGTTTCTGCAACACGAGTCAGCTCATATGCTATGAGATACACTAATATATATGCT	915
Qy	841	TGTGCTGGCAGTCGTCGCAAGTAAACCTTTTCACTTTAAGATGGACTGGATACAAGAT	900
Db	916	TGTGTTGGTGCGGCTCTGTTGATGACTCAATTTACTATCTTTGGCTGGGATATAGTAAAT	975
Qy	901	AGTGATCCCGGATCTAAACGGTATTTGTCATTTGTTGTACAACTAGAACAGTTTACAGACAGT	960
Db	976	AGTCAAGCTGTTCTTAATGGTATTAACAATTTGGTTAAACCACTAGAACAGTTTACAGACAGT	1035
Qy	961	ACCACTGCTGCTACTACTTTTACCAATTCGAATCCAAAGTGTGATTAACCAACCAATTCGAA	1020
Db	1036	ACCACTGCTGCTACTACTTTTACCAATTCGAATCCAAAGTGTGATTAACCAACCAATTCGAA	1095
Qy	1021	ATTTTGCACACTATTTCCAAACCACTACCATCAACCTTCATATGTTGGTGTGACTCTTCC	1080
Db	1096	ATTTTACAACTTATTTCCAAACCTACCAATTTACAACTTCATATGTTGGTGTGACAACTTCC	1155
Qy	1081	TATCTGACTAAGACTGCAACCAATTTGGTGAAAAGCTACTGTTTATTTGTTGATGTCATAT	1140
Db	1156	TACCTGACTAAGACTGCAACCAATTTGGTGAAAAGCTACTGTTTATTTGATGTCATAT	1215
Qy	1141	CATCTACTACCAACTGTTTACAGTGAATGACAGGAAACCAATCACTACTACCACCAACTCGT	1200
Db	1216	CATCTACTACCAACTGTTTACAGTGAATGACAGGAAACCAATCACTACTACCACCAACTCGT	1275
Qy	1201	ACCAATCCAACTGATTCAAATTTGACACAGTGGTGGTACAAGTTCCA	1245
Db	1276	ACCAATCCAACTGATTCCTATAGTACTGTTGGTGGCAAGTTCCA	1320

RESULT 4

US-09-248-796A-20
; Sequence 20, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:

Db 649 AGTCTTGTTGTTCTCTCAGTGACTGCTGGATGATGATCCGGTGTGCTGGATTTTCA 708
QY 601 AGTAGTAACGCTGACGTTGCTATTGATTGCTCAAAATATTCTATATTGTTATCACAAGGA 660
Db 709 GCAACAAAGATGATGACAAATGATTGTTCTACTATACATGTGGGATTAACAATGGT 768
QY 661 TTAATGATTTGAATTTATCCGGTTTCTATCTGAATCATTTAGTTTACACTAAACCTTTGATCA 720
Db 769 TTGAATAGTTGGAATATGCAAGTATCATCAGAAATCATTTTCTTACACCAAACTTTGTACA 828
QY 721 TCTAATGGAATTCAGATTAATATCAAAATGATGCTGCTGTTATGCTGCTCAATTTATTGAT 780
Db 829 CCAACACGTTTTTATTATTACTTATGAATAATGTTCTGCGAGTTATCGTCCATTTATTGAT 888
QY 781 GCTT-----ATATTTCTGCTACAGATGTTAAACCAATATATCTTTAGCATATACCAATGAT 834
Db 889 TCTTACGTAATAAATCAGCAACAGCAAGATGGAATTAATTTGAATTTACAGATATA 948
QY 835 TATACTTTGCTGCGAGTCTGCTGCAAGTAAACCTTTTCACTTTAAGATGACTGGATAC 894
Db 949 TACAATTTGATGGATGGCAAAAGGGAATGATCTCTTATATATCTTTTGGACATCATAC 1008
QY 895 AAGAAATGATGACCGGATCTAAGGTTATGTTGCTATGTTGCTACAACTAGAACAGTTTACA 954
Db 1009 ACAAATAGTATGACGAGTCAATGAGCTGCGGTAGTTGTTACTACGAGAACAGTCACT 1068
QY 955 GACAGTACCACTGCTGCTCACTTTTACCATTTCAATCCAGTGTGATTAACCAACCAAAACA 1014
Db 1069 GATTCTACACAGCAATTTACCACATTTACCGTTTGATCCACAGTTGATAAAACCAAAACC 1128
QY 1015 ATCGAAATTTTGGCAACCTATTCCAAACCACTACCACTTCAATCTTATGTTGGTGACT 1074
Db 1129 ATTGAAGTAATGAAACCATCCCTACTACCACTATTACTTCTATGTTGGGATTTCT 1188
QY 1075 ACTTCTATCTGACTAAGCTGACCAATGCTGAAACAGCTACTGTTATGTTGATGTTG 1134
Db 1189 ACTTCACCTTCTACGAGACTGCACTATTGAGGAAACAGCAACTGTTGTTGTTGATGTT 1248
QY 1135 CCATATCATCTACCAACACTGTTACCACTGATGAGGAGCAAGCAATCACTACCAACCA 1194
Db 1249 CCCTATCATCAACCTACCACTATCACTAGTATATGAGCTGATCACTACCAATCAAGT 1308
QY 1195 ACTCGTACCAATCCAACTGATTCATTCACACAGTGGTGGTACAAAGTTTCCA 1245
Db 1309 ACTTATACAAATCCCACTGACTCGATTGATACAGTTGTTGTACAAAGTTCCA 1359

RESULT 6
US-09-248-796A-2142
; Sequence 2142, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 2142
; LENGTH: 900
; TYPE: DNA
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (866)
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unkno
US-09-248-796A-2142

Query Match 40.9%; Score 509.8; DB 4; Length 900;
Best Local Similarity 82.3%; Pred. No. 1.9e-124;
Matches 610; Conservative 0; Mismatches 127; Indels 4; Gaps 2;
QY 506 CTTCCAGAGTTATGCCAAGTCTCAATAAGGTCAAACTCTTTTTTGTGGC-ACCACAATGT 564
Db 1 CGTCAAGACTTATTTCCAAAGTATTAAACAAAGCTTCAATCACTTATGTGGCAACCAATGT 60
QY 565 GAAAAATGTTTACACATCTCGGTACAAATGGGGTCTTCCAGTAGTAAACGGTGTGCTATT 624
Db 61 GCAAAATGGCTACACATCTCGGTGCAATGGGGTTCATAGTTCTCACTGCTGACACTATT 120
QY 625 GATTGCTCAAAATTTCAATTTGGTATCACAAGGATTAATGATGGAATTTATCCGGT 684
Db 121 GACTGTTCAAAATGTTCAATTTGGTATTAACAAGGGGATTAATGATGGAATTTTCCGGTA 180
QY 685 TCATCTGAATCATTAGTTTACACTTAAACCTTTGATCATCTAATGGAATTCAGATTAATAT 744
Db 181 TCTTCTGATTCATTAAGTTTAAATTAACCTTTGATCATCTAAGGATTTCTATCACAAT 240
QY 745 CAAAAATGATCTGCTGTTATCGTCCATTTTATTTGATGCTTATTTCTGCTACAGATGTT 804
Db 241 GAAATGTTCCCGCTGTTATCGTCCATTTTGGACGTATATATCTCTGGTGTGACAGCAG 300
QY 805 AACCAATATCTTTAGCATATACCAATGATTAATCTTGTGCTGGCAGTCTGCTGCAAGT 864
Db 301 AACAGACA---ATTAAATATATCTAATGATTTATGCTGTGTGGTAGTTCTTTACAAAGT 357
QY 865 AAACCTTTCACTTTAAGATGACTGGATACAAAGATAGTATGATCGCGATCTTAACGGTATT 924
Db 358 AAGCGTTCAATTTAAGATTTGAGAGGATACAAATAGTAGGAAGCTAATTTCTTAACGGTTT 417
QY 925 GTCAATGTTGTACAACTAGAACAGTTTACAGACAGTACCCTGCTGTCACTACTTTTACCA 984
Db 418 GTCAATGTTGTACAAACCGGACAGTTTACTGACAGTACTACTGCTGTCACTACTTTTACT 477
QY 985 TTCAATCCAAAGTGTGTATAAAACCAAAACCAATCGAAATTTTGGAACTTATTCACACCT 1044
Db 478 TTTAATCCAAAGTATTGACAAACCAAAACCAATCGAAATTTTGGAACTTATTCACACCT 537
QY 1045 ACCATCAAACTTCAATGTTGTTGCTGACTTCTTCTATCTGATAGACTGACCAATTT 1104
Db 538 ACTATCAAACTTCAATGTTGTTGCTGACTTCTGATACCTTCTGATACCTTAAACCTGCA 597
QY 1105 GGTCAAAACAGCTACTGTTTATTTGATGTTGCTGATGCTATCATCTACCAACACTGTTAC 1164
Db 598 GGTGAAACAGCTACTGTTTATTTGATGTTGCTGATGCTATCATCTACCAACACTGTTAC 657
QY 1165 GAATGGACAGGAACAACTACCTACCAACCACTGCTGATCAATCCAACTGATTCATTTGAC 1224
Db 658 GAATGGACAGGAACAACTACCTACCAACCACTGCTGATCAATCCAACTGATTCATTTGAC 717
QY 1225 ACAGTGGTGTGCAAGTTCCA 1245
Db 718 ACTGTCGTTGTGCAAGTTCCA 738

RESULT 7
US-09-248-796A-2595
; Sequence 2595, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBIC
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208

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; SEQ ID NO 2595
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-2595

Query Match      33.3%; Score 414.6; DB 4; Length 690;
Best Local Similarity 81.1%; Pred. No. 2e-99;
Matches 494; Conservative 0; Mismatches 114; Indels 1; Gaps 1;

QY 7 ATCACTGGTGTGTTTTCATAGTTTAAATTCATTAACCTGCTCCCAATGCTGCTAAATTAGCT 66
DB 82 ATTACGGGTGTTTTCATAGTTTTCATAGTTTTCATAGTTTTCATAGTTTTCATAGTTTTCAT 141
QY 67 TTCAAAGGGCCAGGATACCCAACTTGGAAATGCTGTTTGGGGTGGTCTTATAGATGGTACC 126
DB 142 TATTAAGGGCCCAATATAGACCAACTTGGAAATGCTGTTTGGGGTGGTCTTATAGATGGTACT 201
QY 127 AGTGCCAAATCCAGGGGATACATTCACATGGAATATGCCATGCTGTTTAAATATATCTACT 186
DB 202 AGTGCAAAATCCAGGAGACATTCACATGGAATATGCCATGCTGTTTAAATATATCTACT 261
QY 187 TCACAAACATCTGTTGATTTTAACTTACCTCCGATGGTGTAAATATGCTACTTGTCAATTTTAT 246
DB 262 GATCAAAACATCTGTTGATTTGACTGCTGAAGGTGTAAATATGCTACTGATGCTTTTAT 321
QY 247 TCTGGTGAAGAAATTCACAACTTTTTCTACATTAACATGCTACTGTGAACGACGCTTTGAAA 306
DB 322 TCAGGTGAAGAAATTTACAACTTTTCTTCATTTAAATGTAATGTAATGTAATGTAATGTAAT 381
QY 307 TCATCCATTAAGGCAATTTGGTACAGTTACTTTTCAATTCATTCATTCATTCATTCATTCAT 366
DB 382 TCATCTATTAAAGGCTTTGGTACGGTTACTTTTACCCTTTTCAATTTTCAATTTTCAATTTTCA 441
QY 367 GGTTCATCACTGATTTGGAAGATCTTAAATGTTTTTACTGCTGTTACCAATACAGTACACA 426
DB 442 GGTTCATCGGTTGATTTGGAAATTTCTCAATGTTTTTAAAGGCTGGCCACCAACACAGTTACT 501
QY 427 TTTTAATGATGGTGAATAAGATATCTCAATTTGATGTTTGAAGGCTCAACCGTTGAT 486
DB 502 TTTTAATGATGGTGAATAAGAAATCTCAATTTGACGTTGTTTGAAGGCTCAACCAAGAT 561
QY 487 CCAAGTGCAATTTGATGCTTCCAGAGTTATGCCAAGTCTCAATTAAGGTCACAACTCTT 546
DB 562 GCAAGTGGAATTTTCATAGCTCAAGCTTATTTCCAGTATTAACCAAGCTTCAATCACT 621
QY 547 TTTTGTGC-ACCAATATGAAATGGTTACACATCTGTTACCAATGCGGTTCTCCAGTAG 605
DB 622 TATGTGCAACCAACCAATGTGCAATGGCTTACACATCTGTTGCAATGGGTTTCTATAGTTCT 681
QY 606 TNAAGGTGA 614
DB 682 CACTGGTGA 690

RESULT 8
US-09-248-796A-2141
; Sequence 2141, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248, 796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074, 725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096, 409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 2141
; LENGTH: 2436

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Db 1045 TCCATTACCAAGCACTTACCACTATACCTTTCATTTCCGACCTCCAGAAAACCAAACT 1104
Qy 1018 GAAATTTTGGCACTTATCCCACTTACCACTTCACTTCACTTATGTTGGTGGTACT 1077
Db 1105 CTAGCTTTAGAGCCCATACCCACCACTACGGTAACAACCTTCCACCACTGGCTTTGAT 1164
Qy 1078 TCCTATCTGACTTAAGACTGCACTCACTTGGTGAACAGCTACTGTTATTTGATGTCGA 1137
Db 1165 TGGTATATATCTAGAGAGCCACCATTTGGTGACACAGCTACTGTTTCAITGATTTCCA 1224
Qy 1138 TATCATCTACCACTGTTTACCACTGAATGGAAGGAGCACTCACTTACCACTCACT 1197
Db 1225 CAACATACAGCTACTTCTTGACCACTATTTGGCAAGAACTCAAGTACAGCGCACTCACT 1284
Qy 1198 CGTACCATCCACTGATTCATTTGACACAGCTGGTGTACAGTTCCA 1245
Db 1285 TACTTCGATGACATAGACTTGGTGGATCTGTCTGATTTGGAATAATTTCCA 1332

RESULT 9

US-09-248-796A-19
; Sequence 19, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR FILING DATE: 1998-02-13
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-19

Query Match 23.6%; Score 293.2; DB 4; Length 699;
Best Local Similarity 75.5%; Pred. No. 2e-67;
Matches 364; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

Qy 1 AAGACAATCACTGGTGTGTTTATGATGTTTAACTTAATCACTTGTGTCCTCAATGCTGCTAAT 60
Db 211 AAAAATACTTACTGGTGTGTTTCAATAGTTTGTGACTCAATGACATGGACTAGATCCGTTGAA 270
Qy 61 TATGCTTTCAAGGCCGAGGATACCAACTTGGAAATGCTGTTTGGTGGTGGTCTAGAT 120
Db 271 TATGTTTCAAGAGGACCGAGAGACTCAACTTGGAAATGCACTTATAGGTTGGTGGTCTTAAAT 330
Qy 121 GGTACAGTGCCTAATCCAGGGGATACATTCATTTGAATATGCTGATGCTGTTTAAATAT 180
Db 331 AGTACACTGCTGACCCAGGAGACATTCACATTTGATTTGCTGCTGTTGCTGTTTAAATTT 390
Qy 181 ACTACTTCAACAACTCTGTTGATTTAACTGCGGATGGTGTGTTAAATGCTACTTGTCAA 240
Db 391 ATAACATCCCAACATCTGTTGATTTGATGCTGATGTTGTTAGCTATGCTGCTGCTGCTG 450
Qy 241 TTTTATCTGGTGAAGAATTCACAACTTTTCTACATTAACATGATGCTGCTGCTGCTGCTG 300
Db 451 TTTAATGCTGGTGAAGAATTTACGACATTTTCTCTTATCATGATGATGCTGCTGCTGCTG 510
Qy 301 TTGAATCATCCATAAGGCAATTTGCTGACATTTCTTACCAATTTGCAATTCATGCTGCT 360
Db 511 TCGGTATCATATGCTAGGGTGTCTGCTAGGGTCAATTTGCCATTTACATTTCAATGATG 570
Qy 361 GGAACAGGTTTCACTCACTGATTTGGAAGATTTCTAAATGTTTCTGCTGCTGCTGCTGCT 420
Db 571 GGAACAGGTTTCTAGTTGATTTGGCAGATTTCCAAATGTTTCTGCTGCTGCTGCTGCTG 630

Qy 421 GTCACATTTAATGATGATGAATAAGATATCTCAATGATGATGATGATGATGATGATGATGAT 480
Db 631 GTGACTTTTCATGATGCGGATACAAAGATTTCTACCACTGTTGATTTTGACGCGCTCTCCA 690
Qy 481 GT 482
Db 691 GT 692

RESULT 10

US-09-248-796A-16
; Sequence 16, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR FILING DATE: 1998-02-13
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-16

Query Match 20.4%; Score 253.6; DB 4; Length 462;
Best Local Similarity 73.2%; Pred. No. 4.6e-57;
Matches 325; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

Qy 688 TCTGAATCACTTGTAGTACACTTAAACCTGTGTACATCTAATGAATTCAGATTAATATCA 747
Db 19 TCAGAAATCAATTTCTTACACGAAACCTGTGTACGTCAACCACTATTTACAGTTGAATTTCA 78
Qy 748 AATGTACTCTGCTGTTATCTGTCATTTATTTGATGCTTATATTTCTGCTACAGATGTTAAC 807
Db 79 AATGTTCTGCTGGGTATCGCCCTTTTGTGATGATATATTTCTGCGAATAATATTTGAT 138
Qy 808 CAATATATCTTTAGCATATACCAATGATATATCTGCTGTCGCTGCTGCTGCTGCTGCTGCT 867
Db 139 AATATATCTTGTAGCTACGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 198
Qy 868 CTTTTCATTTAAGATGGACTGGGATACAAGATAGTGAATGCGGATCTAAGCGTATTTGTC 927
Db 199 CCAITTTACTTTTAACTGCTGGGGGTATATAAACTCTGAAGCAGACTCTGACGGGATGTG 258
Qy 928 ATTGTTGCTACACTAGAACAGTTTACAGACAGTACCACTGCTGCTGCTGCTGCTGCTGCTGCT 987
Db 259 ATCGTAGTTTACCAACAGAACTGTCTACAGACAGTACCACTGCTGCTGCTGCTGCTGCTGCT 318
Qy 988 AATCCAGTGTGTTGATAAAACCAAAACCAATCGAAATTTTGCAACCTATTTCAACCACTACC 1047
Db 319 AATCCAGTGTGATAAAACCAAAACCAATCGAAATTTTGCAACCTATTTCAACCACTACC 378
Qy 1048 ATCAAACTTCAATGTTGGTGTGATCTATCTTCTATCTGATTAAGACTGACCAATTTGCT 1107
Db 379 ATTACAACTTCAATGTTGGTGTGATTTTCCACTTCTTATGAAACATTTAACCGGAACAATTT 438
Qy 1108 GAAACAGCTACTGTTTATTTGTTGAT 1131
Db 439 GGTACTGCGACAGTCAATTTGCTGAT 462

RESULT 11

US-09-248-796A-9483/c
; Sequence 9483, Application US/09248796A
; Patent No. 6747137

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/ GENERAL INFORMATION:
/ APPLICANT: Keith weinstock et al
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
/ TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 107196.132
/ CURRENT APPLICATION NUMBER: US/09/248,796A
/ CURRENT FILING DATE: 1999-02-12
/ PRIOR APPLICATION NUMBER: US 60/074,725
/ PRIOR FILING DATE: 1998-02-13
/ PRIOR APPLICATION NUMBER: US 60/096,409
/ PRIOR FILING DATE: 1998-08-13
/ NUMBER OF SEQ ID NOS: 28208
/ SEQ ID NO 9483
/ LENGTH: 294
/ TYPE: DNA
/ ORGANISM: Candida albicans
/ US-09-248-796A-9483

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Query Match	12.0%;	Score 149.8;	DB 4;	Length 294;
Best Local Similarity	73.9%;	Pred. No. 8.5e-30;		
Matches 190;	Conservative 0;	Mismatches 67;	Indels 0;	Gaps 0;
Qy	226	TATGCTACTTGTCAATTTTATTCTGGTGGAAGAATTCCAACACTTTTTCTACATTAACATGT	285	
Dd	293	TATGCCACTTGTGCATTTAAATGCTGGTGAAGAATTTACGACATTTTCTTCCTATCATGT	234	
Qy	286	ACTGTGAACGACCGTTTGAATCATCATTAAGSCATTTTGSTCAGTTTACTTTTACC AAT	345	
Dd	233	ACTGTGAACAGTGTTC CGGTATCATATGCTAGGGTTTCTGTACGGTCAAATTCGCCANT	174	
Qy	346	GCATTTCAATGTTGGTGGAAACAGGTTTCATCAACTGATTTTGAAGANTTCTAATATGTTTTACT	405	
Dd	173	ACATTTCAATGTAGTGGAAACAGGTTCTTCAGTTGATTTGGCAGATTTCCAAATGTTTTACT	114	
Qy	406	GCTGGTACC AATA CAGTCACAATTTAAATGATGGTGATAAAGATATCTCAAATGATGTTTGAG	465	
Dd	113	GCCGGA AAAAACACTGTGAC TTTTCATGGATGGCGATACAAAGATTTCTTACCAC TGTTGAT	54	
Qy	466	TTTGAAAAGTCAACCGT	482	
Dd	53	TTTTGACGCGTCTCCAGT	37	

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RESULT 12
US-08-145-705A-32/c
; Sequence 32, Application US/08145705A
; Patent No. 5489513
; GENERAL INFORMATION:
; APPLICANT: Springer, Wolfgang; Plempel, Manfred;
; APPLICANT: L bberding, Antonius
; TITLE OF INVENTION: SPECIFIC GENE PROBES AND
; TITLE OF INVENTION: PROCESSES FOR THE DIAGNOSTIC
; TITLE OF INVENTION: INVESTIGATION OF CANDIDA
; TITLE OF INVENTION: ALBICANS
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPRUNG HORN KRAMER & WOODS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
; COMPUTER: NEC PowerMate 1 Plus
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,705A
; FILING DATE: October 28, 1993
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: German P 42 36 708.5

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: FILING DATE: October 30, 1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Kurt G. Briscoe
: REGISTRATION NUMBER: 33,141
: REFERENCE/DOCKET NUMBER: Bayer 8885-KGB
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (914) 332-1700
: TELEFAX: (914) 332-1844
: TELEX:
: INFORMATION FOR SEQ ID NO: 32:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 100 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Candida albicans
: US-08-145-705A-32

Query Match 6.8%; Score 82.4; DB 1; Length 100;
Best Local Similarity 89.0%; Pred. No. 3.1e-12;
Matches 89; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1119 TGTATTGTTGATGCGCATCATCTACTACCAACTGTTTACCAGTGAATGGACAGGAAC 1178
Db 100 TGTATTGTTGATGTTCCATATCACACTACCAACTGTTTACTAGTGAATGGACAGGAAC 41
Qy 1179 AATCACTACCACCAACTCGTATCCAATCCAAGTATCA 1218
Db 40 AATCACTACTACTACCAACAACAACTAATCCAACAGGTCA 1

```

RESULT 13
US-08-145-705A-34/c
; Sequence 34, Application US/08145705A
; Patent No. 5489513
; GENERAL INFORMATION:
; APPLICANT: Springer, Wolfgang; Plempel, Manfred;
; APPLICANT: L'berding, Aronius
; TITLE OF INVENTION: SPECIFIC GENE PROBES AND
; TITLE OF INVENTION: PROCESSES FOR THE DIAGNOSTIC
; TITLE OF INVENTION: INVESTIGATION OF CANDIDA
; TITLE OF INVENTION: ALBICANS
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSER: SPRUNG HORN KRAMER & WOODS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
; COMPUTER: NEC PowerMate 1 Plus
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,705A
; FILING DATE: October 28, 1993
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: German P 42 36 708.5
; FILING DATE: October 30, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Bayer 8885-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844

TELEX:
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Candida albicans
US-08-145-705A-34

Query Match 6.6%; Score 82.4; DB 1; Length 100;
Best Local Similarity 89.0%; Pred. No. 3.1e-12;
Matches 89; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 919 GGTATTGTCAATTCAGTGTGCTACAACTAGAACAGTTACAGACAGTACCACTGCTGTGCTACT 978
DB 100 GGTATTGTCAATTCAGTGTGCTACAACTAGAACAGTTACAGACAGTACCACTGCTGTGCTACT 41
QY 979 TTACCAATTCAGTGTGCTACAACTAGAACAGTTACAGACAGTACCACTGCTGTGCTACT 1018
DB 40 TTACCAATTCAGTGTGCTACAACTAGAACAGTTACAGACAGTACCACTGCTGTGCTACT 1

RESULT 14

US-08-145-705A-33/c
; Sequence 33, Application US/08145705A
; Patent No. 5489513
; GENERAL INFORMATION:
; APPLICANT: Springer, Wolfgang; Plempel, Manfred;
; APPLICANT: L bberding, Antonius
; TITLE OF INVENTION: SPECIFIC GENE PROBES AND
; TITLE OF INVENTION: PROCESSES FOR THE DIAGNOSTIC
; TITLE OF INVENTION: INVESTIGATION OF CANDIDA
; TITLE OF INVENTION: ALBICANS
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPRUNG HORN KRAMER & WOODS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
; COMPUTER: NEC PowerMate 1 plus
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,705A
; FILING DATE: October 28, 1993
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: German P 42 36 708.5
; FILING DATE: October 30, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Bayer 8885-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; TELEX:
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Candida albicans
US-08-145-705A-33

Query Match 6.1%; Score 76; DB 1; Length 100;
Best Local Similarity 85.0%; Pred. No. 1.5e-10;
Matches 85; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1019 AAATTTTGAACCTATTTCGAACCACTACCACTACCACTACCACTATGTTGGTGTGACTACTT 1078
DB 100 AAATTTTGAACCACTATTTCGAACCACTACCACTACCACTATGTTGGTGTGACTACTT 41
QY 1079 CCTATCTGACTAGACTGCACCACTAATGTTGAAACAGCTAC 1118
DB 40 CCTACAGAACCAACTGTACCAATAGGACAACTGCTAC 1

RESULT 15

US-08-145-705A-36/c
; Sequence 36, Application US/08145705A
; Patent No. 5489513
; GENERAL INFORMATION:
; APPLICANT: Springer, Wolfgang; Plempel, Manfred;
; APPLICANT: L bberding, Antonius
; TITLE OF INVENTION: SPECIFIC GENE PROBES AND
; TITLE OF INVENTION: PROCESSES FOR THE DIAGNOSTIC
; TITLE OF INVENTION: INVESTIGATION OF CANDIDA
; TITLE OF INVENTION: ALBICANS
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPRUNG HORN KRAMER & WOODS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
; COMPUTER: NEC PowerMate 1 Plus
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,705A
; FILING DATE: October 28, 1993
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: German P 42 36 708.5
; FILING DATE: October 30, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Bayer 8885-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; TELEX:
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Candida albicans
US-08-145-705A-36
Query Match 5.5%; Score 68; DB 1; Length 100;
Best Local Similarity 80.0%; Pred. No. 1.9e-08;

	Matches	80;	Conservative	0;	Mismatches	20;	Indels	0;	Gaps	0;
Qy	719	CATCTAATGGAATTCAGATTAAATATCAAAATGTACCTGCTGTTATCGTCCATTATTG 778								
Db	100	CATCTAATGGTAICTCTATCACATATGAAATATCCCTGCAGGTTATCGTCCATTATTG 41								
Qy	779	ATGCTTATATTTCTGCTACAGATGTTAACCAATATACTTT 818								
Db	40	ACGTTTATGTATCTGCTCCGGAIGTTAAACAGTATATTTT 1								

Search completed: March 24, 2005, 06:07:24
Job time : 182 secs

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OM protein - protein search, using sw model

Run on: September 8, 2005, 17:51:23 ; Search time 182 Seconds
(without alignments)
2677.572 Million cell updates/sec

Title: US-09-715-876-8
Perfect score: 6495
Sequence: 1 MLQQFTLLFLYLSASAKTI.....SLIQHSTWLYGLTLLSLFI 1260

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	6465	99.5	1260	7 ABW01168	Abw01168 Candida a
2	4204.5	64.7	1119	7 ABW01170	Abw01170 Candida a
3	3938.5	60.6	1047	7 ABW01175	Abw01175 Candida a
4	2680.5	41.3	1443	7 ABW01173	Abw01173 Candida a
5	2584.5	39.8	1270	7 ABW01172	Abw01172 Candida a
6	2452.5	37.8	2297	7 ABW01174	Abw01174 Candida a
7	1992.5	30.7	468	7 ABW01169	Abw01169 Candida a
8	1819	28.0	469	7 ABW01171	Abw01171 Candida a
9	1717.5	26.4	468	7 ABW01176	Abw01176 Candida a
10	939	14.5	1537	8 ADP87475	ADP87475 S cerevis
11	939	14.5	1537	8 ADN18745	ADN18745 Bacterial
12	938	14.4	1537	2 AAR60562	Aar60562 Yeast 4.7
13	932.5	14.4	1322	8 ADN18700	ADN18700 Bacterial
14	721.5	11.1	5179	4 RM24516	Ram24516 C899p pre
15	721.5	11.1	5179	6 ABP55365	Abp55365 Human col
16	721.5	11.1	5179	6 AB007258	Ab007258 Human p53
17	721.5	11.1	5179	7 ADD48091	Add48091 Human Pro
18	721.5	11.1	5179	7 ADD44998	Add44998 Human Pro
19	721.5	11.1	5179	8 ADQ29695	Adq29695 Human col
20	721.5	11.1	5179	8 ADQ80379	Adq80379 Intestina
21	711	10.9	1075	8 AD43638	Ad43638 Bacterial
22	685	10.5	2586	4 AB866878	Ab866878 Drosophil
23	668.5	10.3	778	4 ABU53143	Abu53143 Human tes
24	665	10.2	770	4 ABU53141	Abu53141 Human tes
25	658	10.1	1831	6 ABU43109	Abu43109 Protein e

ALIGNMENTS

RESULT 1

ABW01168
ID ABW01168 standard; protein; 1260 AA.

XX AC ABW01168;

XX XX 15-JAN-2004 (first entry)

XX DE Candida albicans agglutinin-like sequence (ALS) 1 protein.

XX KW Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy; candidiasis; vaccine; fungicide.

XX OS Candida albicans.

XX FN US2003124134-A1.

XX PD 03-JUL-2003.

XX PF 13-SEP-2002; 2002US-00245802.

XX PR 19-NOV-1999; 99US-0166663P.

XX PR 18-NOV-2000; 2000US-00715876.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX FI Edwards JE, Filler SG, Sheppard DC, Ibrahim A, Fu Y;

XX DR WPI; 2003-810971/76.

XX N-PSDB; RAD62305.

XX PT New monoclonal antibody against Candida albicans agglutinin-like sequence
PT 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
PT candidiasis, or to generate an immune response that blocks adherence of
the organism.

XX PS Disclosure; Page 14-17; 65pp; English.

XX CC The present invention relates to a monoclonal antibody against an
XX CC agglutinin-like sequence (ALS)1 protein that specifically binds an
XX CC epitope in an N-terminal domain and which inhibits adherence of Candida
XX CC albicans to endothelial cells. The invention is useful as vaccines for
XX CC treating and preventing disseminated candidiasis and for generating an
XX CC immune response capable of blocking adherence of the organism. The
XX CC invention is also useful in gene therapy. The present sequence is Candida
XX CC albicans agglutinin-like sequence (ALS) protein

XX SQ Sequence 1260 AA;

ABJ19019 Pathogen
Abu53150 Human tes
Abu53149 Human tes
Abu53151 Human tes
Abu53145 Human tes
Abu53148 Human tes
Abu53147 Human tes
Abu53146 Human tes
Abu53142 Human tes
Abp39618 Staphyloc
Ado5656 Staphyloc
Adm72734 Staphyloc
Abp56876 Staphyloc
Abj18914 Pathogen
Aau37120 Staphyloc
Abu16000 Protein e
Abp43908 MUC5B par
Ado58564 Human Gen
Adl23265 Human MUC
Abu53152 Human tes

26 658 10.1 1870 6 ABJ19019
27 657.5 10.1 717 4 ABUS3150
28 657.5 10.1 717 4 ABUS3149
29 657.5 10.1 717 4 ABUS3151
30 657.5 10.1 717 4 ABUS3145
31 657.5 10.1 717 4 ABUS3148
32 657.5 10.1 717 4 ABUS3147
33 657.5 10.1 717 4 ABUS3146
34 655.5 10.1 745 4 ABUS3142
35 651 10.0 2137 5 ABP39618
36 651 10.0 2137 8 ADS05656
37 646.5 10.0 2271 6 ABM72734
38 646.5 10.0 2283 6 ABP56876
39 640.5 9.9 2261 6 ABJ18914
40 640.5 9.9 2344 4 AAU37120
41 637.5 9.8 2271 6 ABU16000
42 632.5 9.7 4315 5 ABP43908
43 624 9.6 800 8 ABO58564
44 618.5 9.5 5703 8 ADL23265
45 615.5 9.5 695 4 ABUS3152

Query Match		99.58;	Score 6465;	DB 7;	Length 1260;	
Best Local Similarity		99.66;	Pred. No. 0;			
Matches 1255;		Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;	
Qy	1	MLQOFTLLFLYLSIASAKTITGVFDSFNSLTWNSAANYAFKPGYPTWNAVLGWSLDGTS	60			
Db	1	MLQOFTLLFLYLSIASAKTITGVFDSFNSLTWNSAANYAFKPGYPTWNAVLGWSLDGTS	60			
Qy	61	ANPGDFTLAMPVCVKYKTTSGTSDVLTADGVKATCOFYSGEBFTPTSTLCTCNDAKLS	120			
Db	61	ANPGDFTLAMPVCVKYKTTSGTSDVLTADGVKATCOFYSGEBFTPTSTLCTCNDAKLS	120			
Qy	121	SIAKFGVTTLPIAFNVCGTSSDLEDSKCFCTAGTNTVTFDGDGKDISIDVEFEKSTVDP	180			
Db	121	SIAKFGVTTLPIAFNVCGTSSDLEDSKCFCTAGTNTVTFDGDGKDISIDVEFEKSTVDP	180			
Qy	181	SAVLIASRVMPSLMKVTLFLVAPOCENGYSCTGTMGFSSNGDVAIDCSNIHIGITKGLND	240			
Db	181	SAVLIASRVMPSLMKVTLFLVAPOCENGYSCTGTMGFSSNGDVAIDCSNIHIGITKGLND	240			
Qy	241	WNYPVSESFYKTCSTNGSIQIKYQNVAGYRPFIDAYISATDVNQYTLAYTNDYTCAG	300			
Db	241	WNYPVSESFYKTCSTNGSIQIKYQNVAGYRPFIDAYISATDVNQYTLAYTNDYTCAG	300			
Qy	301	SRLOSKEPTLRWTCYKNSDAGSGIVATRTVTDSTTAVTTLPEPNSVDKTKTIELQ	360			
Db	301	SRLOSKEPTLRWTCYKNSDAGSGIVATRTVTDSTTAVTTLPEPNSVDKTKTIELQ	360			
Qy	361	PIPTTTITTSVGVTTSYLAKTAPIGETATVIVDVPYHTTTVTSEWGTGTTTTTTRNP	420			
Db	361	PIPTTTITTSVGVTTSYLAKTAPIGETATVIVDVPYHTTTVTSEWGTGTTTTTTRNP	420			
Qy	421	TDSIDTVVQVPLNPFTVSTTEYWSQSFATTTVTAPPGTDTVVIIEPPNHTVTTTEYW	480			
Db	421	TDSIDTVVQVPSNPVSTTEYWSQSFATTTVTAPPGTDTVVIIEPPNHTVTTTEYW	480			
Qy	481	SQSFATTTTVPAPGGTDSVLIIEPPNHTVTTTEYWSQSFATTTVTAPPGTDSVLIIE	540			
Db	481	SQSFATTTTVPAPGGTDSVLIIEPPNHTVTTTEYWSQSFATTTVTAPPGTDSVLIIE	540			
Qy	541	PPNPTVTTTEYWSQSFATTTVTAPPGTDSVLIIEPPNHTVTTTEYWSQSFATTTVT	600			
Db	541	PPNPTVTTTEYWSQSFATTTVTAPPGTDSVLIIEPPNHTVTTTEYWSQSFATTTVT	600			
Qy	601	PPGTDVLIIEPPNHTVTTTEYWSQSFATTTVTGPPSGTDTVVIIEPPNHTVTTTEYW	660			
Db	601	PPGTDVLIIEPPNHTVTTTEYWSQSFATTTVTGPPSGTDTVVIIEPPNHTVTTTEYW	660			
Qy	661	SQSATTTTITAPPGTDTVLIIEPPNHTVTTTEYWSQSFATTTVTAPPGTDTVLIIE	720			
Db	661	SQSATTTTITAPPGTDTVLIIEPPNHTVTTTEYWSQSFATTTVTAPPGTDTVLIIE	720			
Qy	721	PPNHTVTTTEYWSQSFATTTVTAPPGTDTVLIIEPPNHTVTTTEYWSQSFATTTVT	780			
Db	721	PPNHTVTTTEYWSQSFATTTVTAPPGTDTVLIIEPPNHTVTTTEYWSQSFATTTVT	780			
Qy	781	PPGTDVLIIEPPNHTVTTTEYWSQSFATTTVTGPPSGTDTVVIIEPPNHTVTTTEYW	840			
Db	781	PPGTDVLIIEPPNHTVTTTEYWSQSFATTTVTGPPSGTDTVVIIEPPNHTVTTTEYW	840			
Qy	841	SSDGMLLSSTLVTSETTTTLICDGCBSRLSSSGIVTNPPNSSESSIVTSVTPAST	900			
Db	841	SSDGMLLSSTLVTSETTTTLICDGCBSRLSSSGIVTNPPNSSESSIVTSVTPAST	900			
Qy	901	MSDSLSTDGIATSSDNVSKSGSVTTTSTVTTIQTTPNPLSSVTSLTQLSSIPVSE	960			
Db	901	MSDSLSTDGIATSSDNVSKSGSVTTTSTVTTIQTTPNPLSSVTSLTQLSSIPVSE	960			
Qy	961	SESKVTTTNGDNGSGTHDSQSSTTEIEIVTTSSTKVLPPVSSNTDLTSEPTNTREOPT	1020			
Db	961	SESKVTTTNGDNGSGTHDSQSSTTEIEIVTTSSTKVLPPVSSNTDLTSEPTNTREOPT	1020			
Query Match		64.78;	Score 4204.5;	DB 7;	Length 1119;	
Best Local Similarity		64.96;	Pred. No. 4.8e-209;			
Matches 844;		Conservative 106;	Mismatches 128;	Indels 223;	Gaps 18;	
Qy	1	MLQOFTLLFLYLSIASAKTITGVFDSFNSLTWNSAANYAFKPGYPTWNAVLGWSLDGTS	60			
Db	1	MLQOFTLLFLYLSIASAKTITGVFDSFNSLTWNSAANYAFKPGYPTWNAVLGWSLDGTS	60			
RESULT 2						
ABW01170						
ID	ABW01170	standard; protein; 1119 AA.				
XX	XX					
AC	ABW01170;					
XX	XX					
DT	15-JAN-2004	(first entry)				
XX	XX					
DE	DE	Candida albicans agglutinin-like sequence (ALS) 3 protein.				
XX	XX					
KW	KW	Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;				
KW	KW	candidiasis; vaccine; fungicide.				
XX	XX					
OS	OS	Candida albicans.				
XX	XX					
PN	PN	US2003124134-A1.				
XX	XX					
PD	PD	03-JUL-2003.				
XX	XX					
PF	PF	13-SEP-2002; 2002US-00245802.				
XX	XX					
PR	PR	19-NOV-1999; 99US-0166663P.				
PR	PR	18-NOV-2000; 2000US-00715876.				
XX	XX					
PA	PA	(HARB-) HARBOR-UCLA RES & EDUCATION INST.				
XX	XX					
PI	PI	Edwards JE, Filler SG, Sheppard DC, Ibrahim A, Fu Y;				
XX	XX					
DR	DR	WPI; 2003-810971/76.				
DR	DR	N-PSDB; AAD62307.				
XX	XX					
PT	PT	New monoclonal antibody against Candida albicans agglutinin-like sequence				
PT	PT	1 adhesin proteins, for use as a vaccine to treat or prevent disseminated				
PT	PT	candidiasis, or to generate an immune response that blocks adherence of				
PT	PT	the organism.				
XX	XX					
PS	PS	Disclosure; Page 21-23; 65pp; English.				
XX	XX					
CC	CC	The present invention relates to a monoclonal antibody against an				
CC	CC	agglutinin-like sequence (ALS)1 protein that specifically binds an				
CC	CC	epitope in an N-terminal domain and which inhibits adherence of Candida				
CC	CC	albicans to endothelial cells. The invention is useful as vaccines for				
CC	CC	treating and preventing disseminated candidiasis and for generating an				
CC	CC	immune response capable of blocking adherence of the organism. The				
CC	CC	invention is also useful in gene therapy. The present sequence is Candida				
CC	CC	albicans agglutinin-like sequence (ALS) protein				
XX	XX					
SQ	SQ	Sequence 1119 AA;				
Query Match		64.78;	Score 4204.5;	DB 7;	Length 1119;	
Best Local Similarity		64.96;	Pred. No. 4.8e-209;			
Matches 844;		Conservative 106;	Mismatches 128;	Indels 223;	Gaps 18;	


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121 SIKAFGTVTLPIAFNVGGTSSDLEDSKCFIAGTNTVTFDNGDQXIDIVEPEKSTVDP 180
121 SIKALGTVTLPIAFNVGGTSSDLEDSKCFIAGTNTVTFDNGDQXIDIVEPEKSTVDP 180
181 SAYLYASRVNPSLNKVTTLFVAPQCENGYTSGTMGFSSNGDVAIDCSNIHIGITKGLND 240
181 KGYLTDSDRVIPSLNKNVSTLFAVPCANGYSGTMGFANTYGDVQIDCSNIHVGITKGLND 240
241 WNPVSSSESYKTKCTCSNGIQKYQNVAGYRPFDDAYISATDVNQYTLAYTNDYTCAG 300
241 YNPVSSSESYKTKCTCSNGIFITYKNVAGYRPFDDAYISATDVNSYTLAYANEYTCAG 300
301 SRLQSKPTLRWTCYKNSDAGSNGIVATVTRVTDSTTAVTTLFPNPSVDKTKTIELQ 360
301 GYQRAEPTLYRYGYRNSDAGSNGIVATVTRVTDSTTAVTTLFPDNRDKTKTIELK 360
361 PIPFTTITTSYGVGVTTSYLTAKTAPIGETATVIVDVPHYHTTTVTSEWGTGTTTTTNTNP 420
361 PIPFTTITTSYGVGVTTSYLTAKTAPIGETATVIVDVPHYHTTTVTSEWGTGTTTTTNTNP 420
421 TDSIDTVVQVPLNPVSTTEYWSQSFATTTVTAPPGTDTVVIIEPPNHTVTTTEYW 480
421 TDSIDTVIVQVPSNPVSTTEYWSQSFATTTVTAPPGTDTVVIIEPPNHTVTTTEY 480
481 SQSFATTTVTAPPGTDSVLIIEPPNPTVTTTEYWSQSFATTTVTAPPGTDSVLIIE 540
481 SESYTTTSTTAPPGTDSVLIIEPPNPTVTTTEYWSQSFATTTVTAPPGTDSVLIIE 540
541 PPNETVTTTEYWSQSFATTTVTAPPGTDSVLIIEPPNHTVTTTEYWSQSFATTTVT 600
541 PPNETVTTTEYWSQSFATTTVTAPPGTDSVLIIEPPNHTVTTTEYWSQSFATTTVT 600
601 PPGTDTVVIIEPPNHTVTTTEYWSQSFATTTVTAPPGTDSVLIIEPPNHTVTTTEY 660
601 PPGTDTVVIIEPPNHTVTTTEYWSQSFATTTVTAPPGTDSVLIIEPPNHTVTTTEY 660
661 SQSFATTTVTAPPGTDTVLIIEPPNHTVTTTEYWSQSFATTTVTAPPGTDTVLIIE 720
625 SQSFATTTVTAPPGTDTVLIIEPPNHTVTTTEYWSQSFATTTVTAPPGTDTVLIIE 684
721 PPNETVTTTEYWSQSFATTTVTAPPGTDTVLIIEPPNHTVTTTEYWSQSFATTTVT 780
685 PPNETVTTTEYWSQSFATTTVTAPPGTDTVLIIEPPNHTVTTTEYWSQSFATTTVT 744
781 PPGTDTVVIIEPPNHTVTTTEYWSQSFATTTVTAPPGTDTVLIIEPPNHTVTTTEY 840
745 PPGTDTVVIIEPPNHTVTTTEYWSQSFATTTVTAPPGTDTVLIIEPPNHTVTTTEY 776
841 SSDGMLLSSLTVLTESETTTELICDGKESRSLSSSGIVTNPDNSBESSIVTSTVPTAST 900
777 -----LYSTTVYVETKTIITETSCGKGSYVSSTRVITPNNIETPMWNTVDSVTT 830
901 MSDLSSTDGIASATSDNVKSGSVVTTTS-VTTIQTTPNPLSSSVTSLTQLSSIPSVS 959
831 ESTS-QSPSGI-----FSESGSVVETESSTVTTAQTN-----PSVP 865
960 ESESKVFTSNGDNQSGTHDSQSTSEIEIVTTSKVLPPVVSNTDLTSEPTNTEQP 1019
866 TTESEVEFTTKGNNGNGPYESPSTH-----VKSSMDENSEFT----- 902
1020 TTLSTNSNITEDITTSQPTGNDGNTSSTNPVPTVATSTLASASEEDNKGSGHESASTS 1079
903 -----TSTAAS----- 908
1080 LKPSMGENGSLTSTEIE---ATTSTPEAPSPAVSGTDTVTTEPTDTRBQPTTLSTTSK 1136
909 -----TSTDENATIAITGSVEASSPIISSADET-----ATTITTAET 946
1137 TNSELVATTQATNEN-CGKSPSTDLTSSLTGTASTSANSSELYTSVSGTVGAVASASND 1195
947 STSVI---EQPTNNNGGKAPSA-----TSSPSTTTTANNDVSVITG-----TTSTN 989
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QY 1196 QSHSTSVTMSNIVSNTPOTTLSQQVTSSTSPSTNTPIASTYDGSIIQHSWLYGLITL 1255
Db 990 QSQSQSQSN-----SDTQOTLSQQWTSLSVSLH--MLTTFDGSVGIQHSYLCGLITL 1042
QY 1256 LSLFI 1260
Db 1043 LSLFI 1047

RESULT 4
ABW01173
ID ABW01173 standard; protein; 1443 AA.
XX
AC ABW01173;
XX
DT 15-JAN-2004 (first entry)
XX
DE Candida albicans agglutinin-like sequence (ALS) 6 protein.
XX
KW Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;
KW candidiasis; vaccine; fungicide.
XX
OS Candida albicans.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "Encoded by ACG"
XX
PN US2003124134-A1.
XX
PD 03-JUL-2003.
XX
PF 13-SEP-2002; 2002US-00245802.
XX
PR 19-NOV-1999; 99US-0166663P.
PR 18-NOV-2000; 2000US-00715876.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Edwards JE, Filler SG, Sheppard DC, Ibrahim A, Fu Y;
XX
DR WFI; 2003-810971/76.
XX
DR N-PSDB; AAD62310.
XX
PT New monoclonal antibody against Candida albicans agglutinin-like sequence
PT 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
PT candidiasis, or to generate an immune response that blocks adherence of
PT the organism.
XX
PS Disclosure; Page 33-36; 65pp; English.
XX
CC The present invention relates to a monoclonal antibody against an
CC agglutinin-like sequence (ALS)1 protein that specifically binds an
CC epitope in an N-terminal domain and which inhibits adherence of Candida
CC albicans to endothelial cells. The invention is useful as vaccines for
CC treating and preventing disseminated candidiasis and for generating an
CC immune response capable of blocking adherence of the organism. The
CC invention is also useful in gene therapy. The present sequence is Candida
CC albicans agglutinin-like sequence (ALS) protein
SQ Sequence 1443 AA;

Query Match 41.3%; Score 2680.5; DB 7; Length 1443;
Best Local Similarity 43.3%; Pred. No. 4.7e-130;
Matches 629; Conservative 215; Mismatches 387; Indels 223; Gaps 34;

QY 8 LFVLYLSIASAKTITGVDFDSFNLSLTWSNAAYAKGCGYPTWNAVILGSLDGTSANPGDTF 67
Db 9 LPFYCTIAMAKTISGVFTSFNSLTNTGNYPGGPGYPTTAVLGYSLDGTLASPGDTF 68
QY 68 TLNMPCCVKYTTTSQTSVDLTADGVKATCOFYSGEFTTFTSLTCTVNDALKSISKAFGT 127
Db 69 TLVMPCCVKFPIITQTSVDLTANGVKATCTFHAGEDFTTFSSMSCVYVNGLSNIRAFGT 128
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Qy	128	VTLPLAFNVGGTGGSTDLDESKCFAGTAGTNTVTFNDGDKDISIDVBEFKSTVDPSSAYLYAS	187
Db	129	VRLPISFNVGGTGSVNIQDSKCFAGTAGTNTVTFDGHKISTVNFPPKTPQSSSLVYFA	188
Qy	188	RVMSPLNKVTTLFVAQCENGYTSGTWGFPSSNGDVAIDCSNIHIGITKGLNDWNPVSS	247
Db	189	RVIPSLDKLSLWASQCTAGYASGVLFSGATKDDVTIDCSTIHVGITNGLNSYNPVS	248
Qy	248	ESPSYTKTCTGNGIQKONYPAGYRPEIDAYI--SATDVNQYTLAVNDYTCAGSLQS	305
Db	249	ESPSYTKTCTNSPFIITYENYPAGYRPFIDSYVKSATATNGFNLNNTIYNCDGKGN	308
Qy	306	KPFTLRWTGYKNSDAGSNGIVAVTRVTDSTTAVTLPNPNVSDKTKTEILOPIPTT	365
Db	309	DPLIYFTSYNSDAGSNGAAVVVTRVTDSTTAVTLPNPNVSDKTKTEILOPIPTT	368
Qy	366	TITTSYGVGTTSYLTKTAPIGETATVIVDPVPHYTTTTVTSEWGTITTTTTTRNPTDSID	425
Db	369	TITTSYGVGISTSLTKTATIGTATVVDVPHYTTTTTITSYTGSAITTSYTNPTDSID	428
Qy	426	TVVQVPLPNPTVSTTEYWSQSPATTTVAPPDGTDTVIRPNNHVTTEYWSQSPA	485
Db	429	TVVQVSPNPPTVTTQPYSGSVPTTETVTTGPGTDSVIRKBPNNPTVTTIEFYSEFA	488
Qy	486	TITTVTAPPDGTDSVIRPNNPTVTTTEYWSQSPATTTVAPPDGTDSVIRPNNPT	545
Db	489	TTEIVNNPEGDSVIRKBPNNPTVTTIEFYSESPATTTVNNPEGDSVIRPNNPT	548
Qy	546	VTTTEYWSQYATTTVTTAPPDGTDSVIRPNNHVTTEYWSQYATTTVTTAPPDGT	605
Db	549	VTTTEFYSESATTTVTTNYPEGDSVIRPNNPTVTTIEFYSESATTTITNYPEGT	608
Qy	606	DTVIRPNNHVTTEYWSQSPATTTVTPPGDGTDTVIRP-----	649
Db	609	DSVIRPNNPTVTTIEFYSEFVTTETITGTLGTDVIRHDPLESSSSTAIBSSDSN	668
Qy	650	-----PNPTVTTTEYWS-----QSYATTTT	669
Db	669	ISSSAQESSSSVEQSLTGADETSIVELSSRDIPESSIGLTSSESTVSVDYSSTTS	728
Qy	670	ITAPPGETDTVLIRPNNHVTTEYWSQYATTT-----TVPAPPGETD	714
Db	729	ESSIASYDYSSSSIESTLSSDRCSISDITTSFYDSSSDLESTSIYSSSIDAQ	788
Qy	715	TVLIRPNNHVTTEYWSQYATTTVTTAPPDGTDTVIRP-----PNPTV	762
Db	789	SHLVQVSNISISTQELSSSSSEESTP-----ATDALVSSDASSILSSDTSYYPSTI	843
Qy	763	TTTEYW-----SQSPATTT-----TVPAPPGET-DTVIIESSSSKISTS	802
Db	844	SSSDDFPHTIAGESDLSLFIITSTVEISSVSLSITSDPASFDSSSLNLDSSSPSD	903
Qy	803	SNDI-----TSIIIPFS-----RPHVNSITSDLSITPSSSMNTPTSISDGM	845
Db	904	QSDILTSSESPFLVVPFSLSSSSLSLTYPHVNSITVHASSESSSVASPSWASESAN	963
Qy	846	LLSSTLVTESETTELICSDGKE---CSRLLSSSGIVTN-PDSNESSIVTSTVPTASTM	901
Db	964	--DDVTLSSESTDTSSIGTSDSTVTFCCRNDGDCIVTGMPSSSIDSEQTSDDVTTSF	1021
Qy	902	SDLSLSTDG-ISATSSDNV--SKSGVSTTETSVTITQTNPLSSSVTSLSLSTPSV	958
Db	1022	VASSTPTABQITONPNIDISQTSASSTKLUSVSDTVNVSISLSETS--TLSSDDST	1079
Qy	959	SSSEKVTFTSNGD---NQSGTHDSQSTSTIEIIVTTS---STKVLPPVWSSNTDLTSE	1011
Db	1080	S-SDTSISSTNSDGNWAGSSHTSTASIKESSIQKTGVTLSSSVLSTKLSTSDITTE	1138
Qy	1012	PTNTRREQPTTLSTNSITED-----ITTSQP-----TGNG-----DNTGSTNPVPT	1054
Db	1139	LITTELITTELITTELITTEDNEPTFTSTPSSHSIFSSDNLSSKQVDGSESTVEIPPV	1198
Qy	1055	VATSTLASSEENKSGSHESASTSLKPSMGENS-----GLTSTTEIATTTSPTEA-	1106
Db	1199	TDITTVSSVSHSTE-----ASTA-----TLGSEFSKVASAPVNTETSLRSTSSSNHAT	1249
Qy	1107	-----PSPAVSSGT--DVTTEPTDTRQPTTLSTTS-KTNSSELVATTOAT	1148
Db	1250	ESSGTVKSEASABAIPTPTSTNRLSYSTEEBAKGSTYPNSGSTNNLMTESQVAAPTDST	1309
Qy	1149	N--ENGCKSPSTDLTSSLTGTSTASNTSANSSELVTS---GSVTGGAVASANDQS---	1197
Db	1310	SVLTANPVVTSTPDDKSSAAVNQPSKTKSEESIGSLDSVNETNNGFIATLSQSEAPNSL	1369
Qy	1198	-HSTSVT-----NNSNIVSNTPQTLSQOVTSSSPSTNTFFIASTVDGSGSIQH	1245
Db	1370	IHSESIWTMAKTWDASINGDSAAANSQPTLLIQOVATS--SYNQPLITTVAGSSSATKH	1427
Qy	1246	STWLYGLITLLSLP	1259
Db	1428	PSYLLKFIISVALPF	1441
RESULT 5			
ABW01172	standard; protein; 1270 AA.		
ID	ABW01172		
XX	AC	ABW01172;	
XX	DT	15-JAN-2004 (first entry)	
XX	DE	Candida albicans agglutinin-like sequence (ALS) 5 protein.	
XX	KW	Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;	
XX	KW	candidiasis; vaccine; fungicide.	
XX	OS	Candida albicans.	
XX	FN	US2003124134-A1.	
XX	PD	03-JUL-2003.	
XX	PF	13-SEP-2002; 2002US-00245802.	
XX	PR	19-NOV-1999; 99US-0166663P.	
XX	PR	18-NOV-2000; 2000US-00715876.	
XX	PA	(HARB-) HARBOR-UCLA RES & EDUCATION INST.	
XX	PI	Edwards JB, Filler SG, Sheppard DC, Ibrahim A, Pu Y;	
XX	DR	WPI; 2003-810971/76.	
XX	DR	N-PSDB; AAD62309.	
XX	PT	New monoclonal antibody against Candida albicans agglutinin-like sequence	
XX	PT	1 adhesin proteins, for use as a vaccine to treat or prevent disseminated	
XX	PT	candidiasis, or to generate an immune response that blocks adherence of	
XX	PS	the organism.	
XX	PS	Disclosure; Page 27-31; 65pp; English.	
XX	CC	The present invention relates to a monoclonal antibody against an	
XX	CC	agglutinin-like sequence (ALS)1 protein that specifically binds an	
XX	CC	epitope in an N-terminal domain and which inhibits adherence of Candida	
XX	CC	albicans to endothelial cells. The invention is useful as vaccines for	
XX	CC	treating and preventing disseminated candidiasis and for generating an	
XX	CC	immune response capable of blocking adherence of the organism. The	
XX	CC	invention is also useful in gene therapy. The present sequence is Candida	
XX	CC	albicans agglutinin-like sequence (ALS) protein	
SQ	Sequence 1270 AA;		
Query Match 39.8%; Score 2584.5; DB 7; Length 1270;			
Best Local Similarity 45.0%; Pred. No. 3.7e-125;			
Matches 616; Conservative 195; Mismatches 347; Indels 211; Gaps 37;			

CC epitope in an N-terminal domain and which inhibits adherence of Candida
CC albicans to endothelial cells. The invention is useful as vaccines for
CC treating and preventing disseminated candidiasis and for generating an
CC immune response capable of blocking adherence of the organism. The
CC invention is also useful in gene therapy. The present sequence is Candida
CC albicans agglutinin-like sequence (ALS) protein
XX

SQ Sequence 468 AA;

Query Match 30.7%; Score 1992.5; DB 7; Length 468;
Best Local Similarity 80.2%; Pred. No. 4.5e-95;
Matches 376; Conservative 33; Mismatches 59; Indels 1; Gaps 1;
QY 1 MLOQFTLLFLYLSTASAKTITGVDFNSLTWSNAAYAFKGPYPTWNAVLGWSLDGTS 60
DB 1 MLLQFLLLSLCVSVATAKVTGVFNSFSLTWANAASYPYRGPAFTPTWTAIVGWSLDGAT 60
QY 61 ANPGDFTFLNMPGVKFTTQTSVLDLADGVKATCQFYSGEFTTSTLTCTVNDALKS 120
DB 61 ANPGDFTFLNMPGVKFTTQTSVLDLADGVKATCQFYSGEFTTSTLTCTVNDALKS 120
QY 121 SIKAFGTVTLPPIAFNVGSGTSSDLEDSKCFAGTNTVTNDGDKDISIDVBEKSTVDP 180
DB 121 SIKALGTVTLPPIAFNVGSGTSSDLEDSKCFAGTNTVTNDGDKDISIDVBEKSTVDP 180
QY 181 SAYLYASRVMPSLNKKVTLFVAPQCENGYTSGMTGSSNGDVAIDCSNIHIGITKGLND 240
DB 181 SGYFIASRLPSINKVSIITVAPQCENGYTSGMTGSSNGDVAIDCSNIHIGITKGLND 240
QY 241 WNPVSSSEFSYTKTCTSNQIYKQNVAGYRPFIDAYISATDVNQYTLAYNDYTCAG 300
DB 241 WNPVSSDLSYNTKCTSGTSGISYENVPAGYRPFIDAYISATDVNQYTLAYNDYTCAG 300
QY 301 SRLQSKPFTLRWTKYKNSDAGSNGIVIVATRTVTDSTTAVTLTPNPSPVDKTKTIELQ 360
DB 300 SSLQSKPFTLRWTKYKNSDAGSNGIVIVATRTVTDSTTAVTLTPNPSPVDKTKTIELQ 360
QY 361 PIPTTTITTSYGVVTSYLTAKTAPIGETATVIVDPYHTTTVTSEWGTITTTTTRNP 420
DB 360 PIPTTTITTSYGVVTSYLTAKTAPIGETATVIVDPYHTTTVTSEWGTITTTTTRNP 420
QY 421 TDSIDTIVVQVPLNPFTVSTTEYWSQSFATTTTTPAPGGTDSVIIREP 469
DB 420 TDSIDTIVVQVPSNPFTVSTTEYWSQSFATTTTTPAPGGTDSVIIREP 468

RESULT 8

ABW01171
ID ABW01171 standard; protein; 469 AA.

AC ABW01171;

XX 15-JAN-2004 (first entry)

DT 15-JAN-2004 (first entry)

XX Candida albicans agglutinin-like sequence (ALS) 4 protein.

DE Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;

XX candidiasis; vaccine; fungicide.

XX Candida albicans.

OS US2003124134-A1.

XX 03-JUL-2003.

XX 13-SEP-2002; 2002US-00245802.

XX 19-NOV-1999; 99US-0166663P.

XX 18-NOV-2000; 2000US-00715876.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Edwards JE, Filler SG, Sheppard DC, Ibrahim A, Fu Y;

PI

XX WPI; 2003-810971/76.
DR N-PSDB; AAD62308.
XX New monoclonal antibody against Candida albicans agglutinin-like sequence
PT 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
PT candidiasis, or to generate an immune response that blocks adherence of
PT the organism.
XX

PS Disclosure; Page 24-25; 65pp; English.

XX The present invention relates to a monoclonal antibody against an
CC agglutinin-like sequence (ALS) 1 protein that specifically binds an
CC epitope in an N-terminal domain and which inhibits adherence of Candida
CC albicans to endothelial cells. The invention is useful as vaccines for
CC treating and preventing disseminated candidiasis and for generating an
CC immune response capable of blocking adherence of the organism. The
CC invention is also useful in gene therapy. The present sequence is Candida
CC albicans agglutinin-like sequence (ALS) protein
XX

SQ Sequence 469 AA;

Query Match 28.0%; Score 1819; DB 7; Length 469;
Best Local Similarity 72.1%; Pred. No. 4.3e-86;
Matches 338; Conservative 48; Mismatches 83; Indels 0; Gaps 0;
QY 1 MLOQFTLLFLYLSTASAKTITGVDFNSLTWSNAAYAFKGPYPTWNAVLGWSLDGTS 60
DB 1 MLLQFLLLSLCVSVATAKVTGVFNSFSLTWANAASYPYRGPAFTPTWTAIVGWSLDGAT 60
QY 61 ANPGDFTFLNMPGVKFTTQTSVLDLADGVKATCQFYSGEFTTSTLTCTVNDALKS 120
DB 61 ASAGDFTFLDMPGVKFTTQTSVLDLADGVKATCQFYSGEFTTSTLTCTVNDALKS 120
QY 121 SIKAFGTVTLPPIAFNVGSGTSSDLEDSKCFAGTNTVTNDGDKDISIDVBEKSTVDP 180
DB 121 DTAKIGTVTLPPIAFNVGSGTSSDLEDSKCFAGTNTVTNDGDKDISIDVBEKSTVDP 180
QY 181 SAYLYASRVMPSLNKKVTLFVAPQCENGYTSGMTGSSNGDVAIDCSNIHIGITKGLND 240
DB 181 SDRILLRILPSLSQAVNLFVAPQCENGYTSGMTGSSNGDVAIDCSNIHIGITKGLND 240
QY 241 WNPVSSSEFSYTKTCTSNQIYKQNVAGYRPFIDAYISATDVNQYTLAYNDYTCAG 300
DB 241 WNPVSSSEFSYTKTCTSNQIYKQNVAGYRPFIDAYISATDVNQYTLAYNDYTCAG 300
QY 301 SRLQSKPFTLRWTKYKNSDAGSNGIVIVATRTVTDSTTAVTLTPNPSPVDKTKTIELQ 360
DB 301 AASVDSFTHWKGYSNSQAGSNGIIVVTRVTDSTTAVTLTPNPSPVDKTKTIELQ 360
QY 361 PIPTTTITTSYGVVTSYLTAKTAPIGETATVIVDPYHTTTVTSEWGTITTTTTRNP 420
DB 361 PIPTTTITTSYGVVTSYLTAKTAPIGETATVIVDPYHTTTVTSEWGTITTTTTRNP 420
QY 421 TDSIDTIVVQVPLNPFTVSTTEYWSQSFATTTTTPAPGGTDSVIIREP 469
DB 421 TDSIDTIVVQVPSNPFTVSTTEYWSQSFATTTTTPAPGGTDSVIIREP 469

RESULT 9

ABW01176
ID ABW01176 standard; protein; 468 AA.

XX ABW01176;

XX 15-JAN-2004 (first entry)

DT 15-JAN-2004 (first entry)

XX Candida albicans agglutinin-like sequence (ALS) 9 protein.

DE Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;

XX candidiasis; vaccine; fungicide.

XX Candida albicans.

OS

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XX PN US2003124134-A1.
XX PD 03-JUL-2003.
XX XX 13-SEP-2002; 2002US-00245802.
XX XX 19-NOV-1999; 99US-0166663P.
XX XX 18-NOV-2000; 2000US-00715876.
XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX XX Edwards JE, Filler SG, Sheppard DC, Ibrahim A, Fu Y;
XX WPI; 2003-810971/76.
XX DR N-PSDB; AAD62313.
XX XX
XX XX New monoclonal antibody against Candida albicans agglutinin-like sequence
XX PT 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
XX PT candidiasis, or to generate an immune response that blocks adherence of
XX PT the organism.
XX XX
XX PS Disclosure; Page 51-52; 65pp; English.
XX CC
XX CC The present invention relates to a monoclonal antibody against an
XX CC agglutinin-like sequence (ALS)1 protein that specifically binds an
XX CC epitope in an N-terminal domain and which inhibits adherence of Candida
XX CC albicans to endothelial cells. The invention is useful as vaccines for
XX CC treating and preventing disseminated candidiasis and for generating an
XX CC immune response capable of blocking adherence of the organism. The
XX CC invention is also useful in gene therapy. The present sequence is Candida
XX CC albicans agglutinin-like sequence (ALS) protein
XX XX
XX SQ Sequence 468 AA;
XX
Query Match 26.4%; Score 1717.5; DB 7; Length 468;
Best Local Similarity 68.7%; Pred. No. 7.7e-81;
Matches 322; Conservative 69; Mismatches 77; Indels 1; Gaps 1;
QY 1 LMQPTLLFLYLSTIASAKITGVFDSFNSLTWSNANAFKPGYPTWNAVLGSLDQTS 60
DB 1 MLPQFILLFISLTSTAKITGVFNSFDSLTYTRSVAYAYKGPETPTTNAVLYGLNSTT 60
QY 61 ANPGDTFLNWPVCYKTTSTQSVDLTADGVKYATCFYSGEETFTSTLCTVNDALKS 120
DB 61 ADPGDTFLILPCVPKFTTTQTSVDLTADGVSYATCDFNAGEEFTTSSLSCTNSVSVS 120
QY 121 SIKAFGTVTLPAFNVGGTSGSTDLSDSKCTAGTNTVTFTNDGDKDISIDVEFEKSTVDP 180
DB 121 YARVSGTVKLPITFNVGGTSGSVDLADSKCTAGKNTVTFTMDGDKTISTVDFDASVPSP 180
QY 181 SAYLYASRVMPSLNKKVTLFLVAPQCENGYTSCTWGFSSNGDVAIDCSNIHIGTKGLND 240
DB 181 SGYITSSRIIPSLNKLSSLFVVPQCENGYTSCTWGFSSNGDVAIDCSNVNIGISKGLND 239
QY 241 WNPVSSSESYTKTCTENGQIKQYONPAGVRPIDAYISATDVNOYTLATYNDYTCAG 300
DB 240 YNFPVSSSESYTKTCTSTSTVFEQNPAGVRPIDAYISAEINIDKYLTYANEYTCEN 299
QY 301 SRLQSKPTFLRWTKYKNSDAGSNGVIVATRTVTDSTTAVTLFPNPSVDKTKTIELIQ 360
DB 300 GNTVVDPTFLTYGYKNSDAGSDGVIVVTRVTDSTTAVTLFPNPSVDKTKTIELIQ 359
QY 361 PIPTTTITTSYGVVTSYLTAKTAPIGETATVVDVPYHTTTVTSEWGTGTTTTTRTP 420
DB 360 PIPTTTITTSYGVVTSYLTAKTAPIGETATVVDVPYHTTTVTSEWGTGTTTTTRTP 419
QY 421 TSDIIVVQVQPLNPTVSTTHYSQSFAITTTTAPGCGTDTVIREP 469
DB 420 TGSIDTVVQIPSPDPTTTITTEFYGESFASITTTTNPDPGNTSVIIRKP 468
XX
RESULT 10

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ADP87475
ID ADP87475 standard; protein; 1537 AA.
XX
AC ADP87475;
XX
DT 23-SEP-2004 (first entry)
XX
DE S cerevisiae glucan synthase pathway protein YAR050W (FLO1) SeqID17.
XX
KW glucan synthase pathway; RNA expression; protein expression; YOL1 13W;
KW SKM1; YNR066C; YLR121C; YPS3; YHR209W; YKL161C; YFR030W; FLO1; YFR030W;
KW MET10; antifungal agent.
XX
OS Saccharomyces cerevisiae.
XX
PN W02004057033-A1.
XX
PD 08-JUL-2004.
XX
PF 17-DEC-2003; 2003WO-US040532.
XX
PR 19-DEC-2002; 2002US-00324035.
XX
PA (ROSE-) ROSETTA INPHARMATICS LLC.
XX
PI Phillips JW;
XX
WPI; 2004-500308/47.
XX
N-PSDB; ADP87474.
XX
XX
XX Determining whether a molecule affects the function or activity of a
XX PT glucan synthase pathway in a S. cerevisiae cell by determining a change
XX PT in the RNA expression or protein expression in the cell of at least one
XX PT target polynucleotide.
XX
XX Disclosure; SEQ ID NO 17; 132pp; English.
XX
XX This invention relates to a novel method of determining if a molecule
XX CC affects the function or activity of a glucan synthase pathway in a
XX CC Saccharomyces cerevisiae cell which comprises determining if the RNA
XX CC expression or protein expression in the cell of at least one target
XX CC polynucleotide sequence is changed relative to the expression of said
XX CC target polynucleotide sequence in the absence of the molecule. The target
XX CC polynucleotide sequence is selected from the group consisting of YOL1 13W
XX CC (SKM1), YNR066C, YLR121C (YPS3), YHR209W, YKL161C, YFR030W (FLO1) and
XX CC YFR030W (MET10). The method is useful for determining whether a molecule
XX CC affects the function or activity of a glucan synthase pathway in an S
XX CC cerevisiae cell, possibly allowing development of antifungal agents for
XX CC use against a variety of pathogens. The present sequence is that of the
XX CC protein encoded by an S cerevisiae gene which may be used in the method
XX CC of the invention.
XX
XX SQ Sequence 1537 AA;
XX
Query Match 14.5%; Score 939; DB 8; Length 1537;
Best Local Similarity 25.8%; Pred. No. 6.4e-40;
Matches 414; Conservative 246; Mismatches 520; Indels 426; Gaps 84;
QY 2 LQOFTLLFLYLSTIASAKT-----ITGVFDSF-----NSLTWSNANAF----- 40
DB 10 LAVFTLLAL-TSVASGATEACLPAQGRKSGNINIFYQYSLKDSSTSYNNAAYMAYGYASKT 68
QY 41 -----KGPQGYPTW-----NAVLGSLD--G 58
DB 69 KLGSVGGQTDISIDNIPCVSSSGTFFCPQEDSYGNCKGKMGACSNQGIAYWTDLFG 128
QY 59 TSANPGDFTFLNM-----PCVFKYTTSQ-----TSVD 85
DB 129 FYTPTTV-TLEMTGYFLPQTGSGYTKFATVDDSAILSVGATAFNCCAQQQPITSTN 187
QY 86 LTADGVK-----YATCQFYSGEFTTFTSLCTVNDALKSSIKAFGT-----VTLP 131
DB 188 FTIDGKIPWGGSLPPNIEGTVMYAGYYPM-----KVVTYSNAVSWGTLPISVTLP 238
XX

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recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

xx
SQ

Query Match 14.5%; Score 939; DB 8; Length 1537;
Best Local Similarity 25.8%; Pred. No. 6.4e-40;
Matches 414; Conservative 246; Mismatches 520; Indels 426; Gaps 84;

QY 2 LQFTLLFLYLISAKT-----ITGVDFSF-----NSLTWSNAANYAF----- 40
DB 10 LAVFTLLAL--TSVASGATEACLPAGQRKSGNINIFYVSLKDSSTYSNAAYMAYGASKT 68
QY 41 -----KPGGPTW-----NAVLGWSLD--G 58
DB 69 KLGSVGGQDIDINIPCVSSSGTFFCPQSDSYGNMGCKMGACNSQGIAYWSTDLFG 128
QY 59 TSANPGDTFTLNM-----PCVPKYTTSQ-----TSVD 85
DB 129 FYTPTNV-TLEMTGYFLPOTGYSYTFAPATVDDSAILSVGGATFACCAQQPPISTN 187
QY 86 LTADGVK-----YATCFYSGBEFTFTLTCTVDNALKSSIKAFGT-----VTLF 131
DB 188 FTIDGKPMWGLSPNIBGVYVYAGYYP-----KVYNSAVSMGTLFISVTLF 238
QY 132 IAFNVGGSTDLSDSKCFAGTNVTFNDGDKDISIDVEFEKSTV-DPSAYLYASRM 190
DB 239 -----DGTVSDDFEG-----YVVSFDD-----DLSQSNCTVPDPNSYA-VSTTT 277
QY 191 PSLNKVITLFAQCENGYSTGMFSSNGDVAIDCSNIHIGITKGLNDNYPVSSSEF 250
DB 278 TTTEPMTGFTSTSTEMTGTGNGVPTDETVIIRPTTASTIITTEPNWSTFTSTST 337
QY 251 SYTKTCSNGIQKQYONVAGRPIDAYISATDVNQYTLAYTNDYTCAGSLQSKPFTL 310
DB 338 ELTTVGTNGVRTDEII-----VIRPTTATTIITTEPNWSTFTSTSTEL----- 384
QY 311 RWTGVKNSDAGSNGI-----VIVATRTVTDSTTAVTL-PPNPSVDKTKT----- 355
DB 385 -----TTVGTNGLPTDETIIVIRPTTATTATTTTQPNWDTFTSTSTELTTVGTNGL 438
QY 356 -----IELQIPPTTIT-----SYVGVTSYLNKTA-----PIGETATVVDVPPYH 398
DB 439 PTDETIIVIRPTTATTATTTQPNWDTFTSTSTELTTVGTNGLPTDET-IIIRIPTT 497
QY 399 TTT--TVTSEWGTIT-----TTTTRTN--PTDSIDTVVQVPLPNPTVST-----EY 443
DB 498 ATTAMTTTQPNWDTFTSTSTELTTVGTNGLPTD--ETIIIV--IRPTTATTAMTTTQ 552
QY 444 WSQSFAIT-----TTVTAPPG-GTD--TVIIREPPNHT--VTTEYWSQSFAIT-----TTV 490
DB 553 WNDTFTSTSTEMTGTGNGLPTDETIIVIRPTTATTIITTEPNWSTFTSTSTEMT 612
QY 491 TAPPG-GTDS--VIIREPPNHT--VTTEYWSQSFAIT-----TTVTAPPG-GTDS--VII 538
DB 613 TGTNGLPTDETIIVIRPTTATTIITQPNWDTFTSTSTEMTGTGNGLPTDETIIVI 672
QY 539 REPPNHT--VTTEYWSQSFAIT-----TTVTAPPG-GTDS--VIIREPPNHT--VTTEY 587

DB 673 RTPTTATTAMTTQPNWDTFTSTSTELTTVGTGTLPTDETIIVIRPTTATTAMTTTQ 732
QY 588 WSQSFAIT-----TTVTAPPG-GTD--TVIIREPPNHT--VTTEYWSQSFAIT-----TTV 634
DB 733 WNDTFTSTSTEMTGTGNGVPTDETVIIRPTTSEGLISTTTTEPWTGTFTSTSTEMT 792
QY 635 T--GPPSGTDTVIIREPPNHT--VTTEYWSQSFAIT-----TTIAP-----POETDTVLI 682
DB 793 TGTNGLPTDETIIVIRPTTSEGLIVTTTTPWTGTFTSTSTEMTITGTNGVPTDETVIVI 852
QY 683 REPPNHT--VTTEYWSQSFAIT-----TTVTAPPG-GTD--TVIIREPPNHT--VTTEY 731
DB 853 RTPTSEGLISTTTTEPWTGTFTSTSTEMTITGTNGVPTDETVIIRPTTSEGLISTTTEP 912
QY 732 WSQSFAITTTVTAPPGTDT-----TVIIREPPNHT--VTTEYWSQSFAITTTVTAPP 782
DB 913 WTGTFTSTSTEMTGTGNGVPTDETVIIRPTTSEGLISTTTTEPWTGTFTSTSTEMT 972
QY 783 GGT-----DTVIIYSMSSSKI-----STSSNDITSIIPSPRP----- 816
DB 973 TGTNGLPTDETIIVIRPTTSEGLISTTTTEPWTGTFTSTSTEMTITGTNGVPTDETVIVI 1032
QY 817 -----HYNSTTSD-LSTPESSSMPTPSSISDGMLLSSTTLVTESETT-----TELICS 865
DB 1033 RTPTSEGLIVTTTEPWTGTFTSTSTEMTGTGNGLPTDETVIIRPTTITAISSLSSSS 1092
QY 866 DGKCEKRLSSSGIVTNP--DSNESSIVTSTVPTASTMSDSLSTDGISATSDNVKSG 923
DB 1093 SGIITSSITSSRIIT-PFYPSNGTSSVSSSVTSSLTSSPVISSSVISSSTTS 1151
QY 924 VSVTTESTVTIOTTNPLSSSVTLQLSISPSVSESESKVFTFTSNGDNQSGTHDQST 983
DB 1152 TSIFSSSKSV--IPTSSSTSGSESETSSAGSVSS-----SPISSESSKSPYSSSS- 1204
QY 984 STIEIVTST-----KVLPPVSVSSNDLTSTPTWTRQPTTLSTTS-----NSITE 1031
DB 1205 ---LPLVTSATTQETASSLPAPT-----TKTSEQTLIVTVTSCSHVCTESISP 1252
QY 1032 DITTSQPTGNGDNTSTN--PVPTVATSLAGASEDNKSGSHESASTSLKPSMGNSG 1089
DB 1253 AIVSTATVTVSGVTTEYTTWCPISTTETTKGTTEQTTETTKQTTVTVIISSESDVCS 1312
QY 1090 LTTSTEIATTTPTPEAPSPAVSGTDVTTEPTDTRQPTTLST-----SKTNSGLV 1142
DB 1313 KTASPAIVSTATINGVTTEYTTWCPIST--TESRQQTTLVTVTSCSGVCSSETASPAI 1370
QY 1143 ATT-----QATNENGCKSPSTDLSLTTGT--SASTSANSSELVTSVSV 1184
DB 1371 VSTATATVNDVTVYPTWRPQTANESVSSKMSATGETTNTLAAETTTNTVAETITN 1430
QY 1185 TCGA-----VASASNDQSHSTSV-----TNSNSIVNTPTQTLISQ 1220
DB 1431 TGAATKTVVTSLSRSNHAETQTASATDVIGHSSVSVSEIGTNTKSLTSSGLSTWSQ 1490
QY 1221 VTSSP-----STNTFIATSYDGSIIQHSWLYGLITLLSLFI 1260
DB 1491 PRSTPASSVMGYSTASLEISTYAGSANSLLAGSLSVFIASLLIAI 1536

RESULT 12
AAR60562
ID AAR60562 standard; protein; 1537 AA.
XX AAR60562;
AC AAR60562;
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 13-APR-1995 (first entry)
DE Yeast 4.7 kb agglutination gene FLO1L.
KW Yeast; agglutination; FLO1L.
XX

OS Saccharomyces cerevisiae.

XX XX
PN WO9419475-A2.
XX
PD 01-SEP-1994.
XX
PF 24-FEB-1994; 94WO-JP000290.
XX
XX 26-FEB-1993; 93JP-00038871.
PR (SABP) SAPPORO BREWERIES.
XX (PANI-) PANIMOLABORATORIO BRYGGERILABORATORIUM.
PA
XX
PI Watari J, Takata Y, Ogawa M, Penttila M, Onnela M, Keraenen S;
XX WPI; 1994-294338/36.
DR N-PSDB; AAQ71390.
XX
XX New yeast agglutination genes and yeast contg. them - impart
PT agglutination properties to facilitate removal from fermentation media.
XX
XX Disclosure; Page 43-48; 75pp; English.
XX
CC The agglutination gene is called FLO1. Saccharomyces cerevisiae includes
CC an agglutination gene of 4.7 kb (FLO1L) and an agglutination gene of 2.6
CC kb (FLO1S). FLO1L is the intact FLO1 gene on chromosome I, and FLO1S is
CC the FLO1L gene with a portion of the ORF deleted in frame. FLO1L imparts
CC a relatively strong agglutinative property to the host yeast into which
CC it is introduced, while FLO1S imparts a weaker agglutinative property.
CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to
CC correct OS field.)
XX
SQ Sequence 1537 AA;

Query Match 14.4%; Score 938; DB 2; Length 1537;
Best Local Similarity 26.0%; Pred. No. 7.2e-40;
Matches 417; Conservative 244; Mismatches 523; Indels 418; Gaps 85;
QY 2 LQQTLLFLVLSIASAKT-----ITGVDFSF-----NSLTWSNAAYAF----- 40
Db 10 LAVFTLLAL-TSVASGATEACLPAQRKSGNINIFYQSLKDSSTYSNAAYMAYGASKT 68
QY 41 -----KPGGYPTW-----NAVLGMSLD--G 58
Db 69 KLGSVGGOTDISIDYNIPCVSSSGTFPCQEDSYGNWCKGMGACNSQGIAYWSTDLFG 128
QY 59 TSANPGDTFTLNM-----PCVKYITSQ-----TSVD 85
Db 129 FYTTPTNV-TLEMTGYFLPQTGYTFKFAVDSDSAILSVGGATFAFCCCAQQQPPITSTN 187
QY 86 LTADGVK-----YATQFYSGBEFTTFLCTVNDALKSSIKAFGT-----VTLP 131
Db 188 FTIDGKPMWGSLLPNIEGTVMYAGYPM-----KVYVNAVSGTLPISVTL 238
QY 132 IAFNVGGTSGSDLESCKEFTAGTNTVTFNDGDKDISIDVEFEKSTV-DPSAYLYASRVM 190
Db 239 -----DGYTVSDDFEG-----YVVSFDD-----DLSQSNCTVPDPSNYA-VSTTT 277
QY 191 PSLMKVYTLFVAPOCENGYSCTMGFSSNGSDVAIDCSNHIHIGTKGLNDWNPVSSSEF 250
Db 278 TTTFPWTGTFSTSTSTMTVTGTVNGVPTDETVIVIRTPPTASTIITTEPWNSTFTSTST 337
QY 251 SYTKTCTSNQIQKQVNPAGRYPFIDAYISATDVNQYTLAYTNDYTCAGSRQKQPFLL 310
Db 338 ELTTVTGNGVRTDETL-----VIRPTATTAITTEPWNSTFTSTSTEL----- 384
QY 311 RWTGKNSDAGSNGI---VIVATRTVTDSTAVTTL-PNPNSVDKTKT----- 355
Db 385 -----TTVTGTLGTPDETLIVIRTPPTATTAATTTQPNWDTFTSTSTMTVTGTL 438
QY 356 -----TEILOPIPTTIT-----SYGVTTSYLTAKA---PIGETATVIVDVPYH 398
Db 439 FTDETLIVIRPTATTATTAATTTQPNWDTFTSTSTMTVTGTLGTLPTDET-IIIVIRPTT 497

QY 399 TTT--TVTSEWGTIT-----TTTRTN--PTDSIDTVVQVPLNPFT-VSTTEYWSQS 447
Db 498 ATTAMTTTQPNWDTFTSTSTMTVTGTLGTLPTDE-TIIVIRTPPTATTAMTTQPNWDT 556
QY 448 FATT-----TTVTAPPG-GTD--TVIIRPPNHT--VTTEYWSQSFAIT-----TTVTAPP 494
Db 557 FTSTSTMTVTGTLGTLPTDETLIIIVIRPTTATTAITTEPWNSTFTSTSTELTTVTGTL 616
QY 495 G-GTDS--VIIRPPNPT--VTTEYWSQSFAIT-----TTVTAPPG-GTDS--VIIRPP 542
Db 617 GLPTDETLIIIVIRPTTATTAATTTQPNWDTFTSTSTMTVTGTLGTLPTDETLIIIVIRPT 676
QY 543 NPT--VTTEYWSQSFAIT-----TTVTAPPG-GTDS--VIIRPPNHT--VTTEYWSQS 591
Db 677 TATTAMTTTQPNWDTFTSTSTMTVTGTLGTLPTDETLIIIVIRPTTATTAATTTQPNWDT 736
QY 592 YATT-----TTVTAPPG-GTD--TVIIRPPNHTV--TTTEYWSQSFAIT-----TTVT-- 635
Db 737 FTSTSTMTVTGTLGTLPTDETVIIVIRPTSEGLISTTTTEPWTGTFSTSTSTMTVTGTL 796
QY 636 GPPSGTDTVIIRPPNP--TVTTEYWSQSFAIT-----TTITAP-----PGTDTVLIRPP 686
Db 797 GQPTDETVIIVIRPTSEGLVTTTTTEPWTGTFSTSTMTVTGTLGTLPTDETVIIVIRPT 856
QY 687 NHTV--TTTEYWSQSFAIT-----TTVTAPPG-TD--TVIIRPPNHTV--TTTEYWSQS 735
Db 857 SEGLISTTTTEPWTGTFSTSTMTVTGTLGTLPTDETVIIVIRPTSEGLISTTTTEPWTG 916
QY 736 YATT-----TTVTAPPG-GTD--TVIIRPPNHTV--TTTEYWSQSFAITTTVTAPPGT- 785
Db 917 FTSTSTMTVTGTLGTLPTDETVIIVIRPTSEGLISTTTTEPWTGTFSTSTSTMTVTGTL 976
QY 786 -----DTVIIYBSMSSKI-----STSSNDITSLIPSRP----- 816
Db 977 GQPTDETVIIVIRPTSEGLISTTTTEPWTGTFSTSAEMTVTGTNGQPTDETVIIVIRPT 1036
QY 817 --HYNSTSD-LSTPESSMNTPTSISDGMLLGSTLLVTESETT-----TELICSDGKE 869
Db 1037 SEGLVTTTTTEPWTGTFSTSTMTVTGTLGTLPTDETVIIVIRPTTATTAISSLSSSSGQI 1096
QY 870 CSRSLSSSGIVNTP--DSNESSIVTSTVPTASTMSDLSLSDGISATSDNVSKSGSVT 927
Db 1097 TSISITSRPIIT-PFYPSNGTSSVSSSVTSSLTSSPVISSSVISSSTTTSTSTIF 1155
QY 928 TETSVTTIQTENPLSSSVTSLTQLSSIPSVSESESKVFTNGDNQSGTHDSQSSTEI 987
Db 1156 SESSKSSV--IPTSSSTSGSSESETSSAGSVSS-----SFISSSKSPFYSSSS--L 1205
QY 988 EIVTTSST-----KVLPPVVSNTDLTSEPTNTREQPTTLSTTS-----NSITEDIIT 1035
Db 1206 PLVTSATTSQETASSLPPATT-----TKTSEQTLLVTVTSCESHVCTESISPAIVS 1256
QY 1036 SQPTGNGDNTASTN--PVPTVATSTLASASEDNKSGSHESASTSLKPSMGNSGLTIS 1093
Db 1257 TATVTVSGVTEYTTWCPISTTETTKQTGTEQTETTKQTIVTVTSSCESDVCSKTAS 1316
QY 1094 TEATVTTGPTAPSPAVSGTDTVTTEPTDTRREQPTTLSTT-----SKTNSSELVATT- 1145
Db 1317 PALVSTSTATINGVTTEYTTWCPIST--TESRQQTLLVTVTSCESGVCSGSETASPAIVSTA 1374
QY 1146 -----QATNENGGKSPDLDLSLTTGT-SASTSANELSVTSGSVTGA 1188
Db 1375 TATVNDVTVTVTPRQPTANEBSVSSKMSATGETTTNTLAAETTTTVAEAETITNGAA 1434
QY 1189 -----VASANDQSHSTSV-----TNSNSIVNTPTOTLLSQOVTS 1224
Db 1435 ETKTVTVTSSLRSRNNHAETOTASATDVIGHSSSVVSVSETGNTKSLTSSGLSTMSQPRST 1494
QY 1225 SP-----STNTFIASITDYGSGSIIQHSWLXGLITLLSLFI 1260
Db 1495 PASSMVGYSTASLEISTYAGSANSLLAGSLSVFIASLLAI 1536

RESULT 13	
ADN18700	
ID	ADN18700 standard; protein; 1322 AA.
AC	
AC	ADN18700;
XX	
DT	02-DEC-2004 (first entry)
XX	
DE	Bacterial polypeptide #1353.
XX	
KW	Recombinant DNA construct; transformed plant; improved plant property;
KW	cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW	pathogen tolerance; pest tolerance; plant disease resistance;
KW	cell cycle pathway modification; plant growth regulator;
KW	homologous recombination; seed oil yield; protein yield; carbohydrate;
KW	nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW	bacterial polypeptide.
XX	
OS	Bacteria.
XX	
PN	US2003233675-A1.
XX	
PD	18-DEC-2003.
XX	
PF	20-FEB-2003; 2003US-00369493.
XX	
PR	21-FEB-2002; 2002US-0360039P.
XX	
PA	(CAOV/) CAO Y.
PA	(HINK/) HINKLE G J.
PA	(SLAT/) SLATER S C.
PA	(CHEN/) CHEN X.
PA	(GOLD/) GOLDMAN B S.
XX	
PI	CAO Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
DR	WPI; 2004-061375/06.
XX	
PT	New recombinant DNA construct comprising a promoter positioned to provide
PT	for expression of a polynucleotide encoding a polypeptide from a
PT	microbial source, useful for producing plants with improved properties.
XX	
PS	Claim 1; SEQ ID NO 1353; 122pp; English.
XX	
CC	The invention relates to a recombinant DNA construct comprising a
CC	promoter functional in a plant cell, where the promoter is positioned to
CC	provide for expression of a polynucleotide encoding a polypeptide from a
CC	microbial source. The invention also relates to a transformed plant
CC	comprising the recombinant DNA construct and a method of producing a
CC	transformed plant having an improved property. The plant is a crop plant
CC	such as maize or soybean. The method of producing a transformed plant
CC	having an improved property comprises transforming a plant with the
CC	recombinant DNA construct and growing the transformed plant, where the
CC	polynucleotide or polypeptide is useful for improving plant properties.
CC	The recombinant DNA construct is useful for producing plants with
CC	improved plant properties, e.g. improved cold, heat or drought tolerance,
CC	tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC	increased resistance to plant disease, better growth rate by modification
CC	of the cell cycle pathway with plant growth regulators, increased rate of
CC	homologous recombination, modified seed oil or protein yield and/or
CC	content, improved yield by modification of carbohydrate, nitrogen or by
CC	phosphorus use and/or uptake, by modification of photosynthesis or by
CC	providing improved plant growth and development under at least one stress
CC	condition. Improved lignin production or improved galactomannan
CC	production. This sequence represents a bacterial polypeptide used in the
CC	scope of the invention. Note: The sequence data for this patent did not
CC	form part of the printed specification but was obtained in electronic
CC	format from USPTO at seqdata.uspto.gov/sequence.html .
XX	
SQ	Sequence 1322 AA;

Db 949 SSVPTSSSTSGSSESETGSSASAS-----SSSSISSESPKSTYSSSLP-PVTSATTSQEI 1004
QY 952 LSSIPSVSESKVFTFTSNGDQSGTHDSOSTEIEIVTTSKVLPPVVSNTDLTSE 1011
Db 1005 TSSLPPVTTTKT-----SEQTLLVTVTSCSHVCTESISSAIVSTAT 1046
QY 1012 PT---NTREOPTLSTTSNSITDIT-TSOPTGNGDNTSSTNPVPTVATSTILASASEED 1067
Db 1047 VTVSGATTEYTWCPISFTTEITKQTTETKTKTEQTTETTKQITTVVT---ISSCESD 1103
QY 1068 --NKGSGHESASTSLKPSMGENGLTTSIEIAETTSPTPEAPVSSGVDVTEPTDTR 1125
Db 1104 VCSKTASPAIVSTSTATINGVTTEYTWCPISTTESKQQTLLVTVTSCSGVCSETT--- 1160
QY 1126 EQPTTLSTTSKTNSELVAT-----TOATNENGKSPSTDLTSSLTGTCSAST-----SA 1174
Db 1161 -SPAIVSTATATVNDVVTVVTSWRPQTNEQSVSSKMSATSETTNTGHAETTTGTAA 1219
QY 1175 NSELVTSGSVT-----GGAVASASNDQSHSTSV-----TNSNSIVSNTPTQLSQQVTS 1224
Db 1220 ETKTVTVTSISRFNHAETQTASATDVIGHSSVVSVSETGNTKSLTSSGLSTMSQQPRST 1279
QY 1225 -----SPSNWTFIASYDGGSIHQHSTWLYGLITLLSLFI 1260
Db 1280 PASSWVGSTASLEISTYAGSANSLLAGSLGVFIASLLLAI 1321

RESULT 14
AAM24516
ID AAM24516 standard; protein; 5179 AA.
AC AAM24516;
XX
XX 12-OCT-2001 (first entry)
DE C899P predicted amino acid sequence.
KW Human; immunotherapy; diagnosis; colon cancer; colon tumour; immunogenic;
KW gene therapy; vaccine; colonic cancer.
OS Homo sapiens.
XX
XX W0200149716-A2.
XX 12-JUL-2001.
XX 29-DEC-2000; 2000WO-US035596.
XX 30-DEC-1999; 99US-00476296.
PR 10-JAN-2000; 2000US-00480321.
PR 15-FEB-2000; 2000US-00504529.
PR 06-MAR-2000; 2000US-00519444.
PR 19-MAY-2000; 2000US-00575251.
PR 29-JUN-2000; 2000US-00609448.
PR 28-AUG-2000; 2000US-00649811.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Lodes MJ, Secretist H, Benson DR, Meagher MJ, Stolk JA;
PI King GE, Wang T, Jiang Y;
XX
XX WPI; 2001-441847/47.
XX
XX Colon tumor associated proteins and nucleic acids useful for the
PT prevention, diagnosis and treatment of colonic cancer.
XX
XX Claim 2; Page 446-462; 472pp; English.
XX
XX The present invention describes colon tumour associated proteins (I) and
CC the polynucleotides (II) that encode them. (I) have cytostatic activity.
CC (I) and (II) can be used in gene therapy and vaccine production. (I) and
CC (II) may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate colon tumour associated protein (TCAP)

CC expression, such as colonic cancer. For example, (I) and (II) may be used
CC to treat disorders associated with decreased expression by rectifying
CC mutations or deletions in a patient's genome that affect the activity of
CC TCAPs by expressing inactive proteins or to supplement the patients own
CC production of them. Additionally, (II) may be used to produce the TCAP
CC proteins, by inserting the nucleic acids into a host cell culturing the
CC cell to express the protein. (II) and its complementary sequences may
CC also be used as DNA probes in diagnostic polymerase chain reaction (PCR)
CC and hybridisation assays to detect and quantitate the presence of similar
CC nucleic acids in samples, and therefore which patients may be in need of
CC restorative therapy. (I) may also be used as antigens in the production
CC of antibodies against TCAPs and in assays to identify modulators of TCAP
CC expression and activity. Anti-(I) antibodies and antagonists may also be
CC used to down regulate TCAP expression and activity. The anti-(I)
CC antibodies may also be used as diagnostic agents for detecting the
CC presence of TCAPs in samples (e.g. by enzyme linked immunosorbant assay
CC (ELISA)). AAI28460 to AAI29512 and AAM24494 to AAM24523 represent
CC nucleotide and amino acid sequences given in the exemplification of the
CC present invention
XX
XX Sequence 5179 AA;

Query Match 11.1%; Score 721.5; DB 4; Length 5179;
Best Local Similarity 25.3%; Pred. No. 5.2e-28;
Matches 335; Conservative 158; Mismatches 554; Indels 279; Gaps 54;
QY 59 TSANPGDTFTLAMPKCVFKYTTTSQTSVDLTDAGVKYATCQFYSGEETFTSTLTCTVNDAL 118
Db 1647 TTTTPPTTPSPPP-----TTTTPSPPIITTTTPPTT-----TPSSPIITTTSPPT 1693
QY 119 KSSIKAFGTWTLPIAFNVGSGSTDLSDSKCFTAGTNTVTFNDGDKDISIDVEFKSTV 178
Db 1694 TTTTTPSPITTPSSPIITTTTTPSPPTTTPSPPTTTPSPPTTTPSPPTTTPSPPTTTP 1747
QY 179 DP---SAYLYASRVMSLKNVT-----TLFVAPQCE-NGY-TSGTWGSSNGDVA 224
Db 1748 PPTTSSPLTTPPLPSITPTTTPSPPTTTPSPPTTTPSPPTTTPSPPTTTPSPPTTTP 1807
QY 225 IDCSNIHIGITKGLDNWNPVSESEFSY-----TKTC-TSNGIQIKYQN-VPAGY 272
Db 1808 L-----IGDVGCG-PGWAANIISCRATWYPDVIGQLGVTVCDVSVGLICKEDQKPGGV 1860
QY 273 RPFIDAYISATDVNQYTLAYTNDYTCAGSRLOSKPFTLRWTGYKNSDAGSNGIVVATTR 332
Db 1861 IEM-----APCLNVEINVQCC--ECVTQPTTMTTNTTENPTPTTPTTPTTPTTPTT 1907
QY 333 TVTSDTAVTTLFPNPSVDKTKIEILOPIPTTTTTSVGVTTSLTKTAPIG-ETATV 391
Db 1908 TPTPTPTGTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 1967
QY 392 IVDVRYHTTTTPTTSEWGT-----ITTTT-----TRTNPTDSIDTVVVQVP 432
Db 1968 ---TPITTTTTTPTPTPTPTPTPTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 2024
QY 433 LPNPTVSTTEYWSQSFAITTTVTAPGGTDTVIIREPNNHVTTEYWSQSFAITTTVTA 492
Db 2025 TPTPTGTQTP-TTPTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 2072
QY 493 PPGTDP-----SVIIREPNNPTVTTEYWSQSFAITTTVTAP-----PGTD-----S 535
Db 2073 TPTGTQTPPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 2132
QY 536 VIIEPPNPTVTTEYWSQSFAITTTVTAP-----PGGTDVSVIIREPNNHVTTEYWSQS 592
Db 2133 TTTTPTPTPTPTGTQTPPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 2180
QY 593 ATTTTVPAPGGTDTVIIREPNNHVTTEYWSQSFAITTTVTGPPSGTD-----T 643
Db 2181 -TTTPTPTPTGTQT-----PTTPTTPTT-----TTTPTPTPTGTQTPTTPTTPTT 2226
QY 644 VIIEPPNPTVTTEYWSQSFAITTTITAPGETDVLIREPNNHVTTEYWSQSFAIT 703
Db 2227 TTVTPTPTPTGTQTP-TTPTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 2272

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OM protein - protein search, using sw model

Run on: September 8, 2005, 18:17:16 ; Search time 46 Seconds
(without alignments)
2044.735 Million cell updates/sec

Title: US-09-715-876-8
Perfect score: 6495
Sequence: 1 MLQOFTLLFLYLSTASAKTI.....SIHQSTWLYGLTLLSLFI 1360

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues
Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.psp.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.psp.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.psp.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.psp.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.psp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.psp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4190.5	64.5	1191	4	US-09-248-796A-16243
2	3220	49.6	1060	4	US-09-248-796A-14123
3	2779	42.8	780	4	US-09-248-796A-16702
4	2297	35.4	646	4	US-09-248-796A-16701
5	2273	35.0	812	4	US-09-248-796A-16244
6	1994	30.7	511	4	US-09-248-796A-14125
7	1883	28.0	448	4	US-09-248-796A-14116
8	1816	28.0	426	4	US-09-248-796A-14114
9	1808.5	27.8	386	4	US-09-248-796A-14126
10	1634.5	25.2	522	4	US-09-248-796A-14121
11	1500.5	23.1	501	4	US-09-248-796A-14118
12	1206.5	18.6	300	4	US-09-248-796A-16245
13	1138	17.5	240	4	US-09-248-796A-14117
14	940	14.5	1537	1	US-08-325-267A-2
15	815	12.5	229	4	US-09-248-796A-16698
16	797	12.3	171	4	US-09-248-796A-14120
17	761	11.7	823	4	US-09-248-796A-16699
18	721.5	11.1	5179	4	US-09-538-092-1258
19	651	10.0	2137	3	US-09-134-001C-4463
20	648	10.0	176	4	US-09-248-796A-16696
21	640	9.9	232	4	US-09-248-796A-14122
22	583	9.0	154	4	US-09-248-796A-14119
23	553.5	8.5	2870	4	US-09-479-467A-15
24	553.5	8.5	3178	4	US-09-479-467A-4
25	521.5	8.0	1140	4	US-09-538-092-647
26	516	7.9	894	3	US-08-362-525-22
27	516	7.9	894	3	US-08-971-692-15

28	496	7.6	3892	4	US-09-328-352-5503	Sequence 5503, Ap
29	488	7.5	1721	3	US-08-928-361B-6	Sequence 6, Appli
30	488	7.5	1721	4	US-09-588-995A-6	Sequence 6, Appli
31	487	7.5	1721	3	US-08-700-651-5	Sequence 5, Appli
32	487	7.5	1837	3	US-08-928-361B-5	Sequence 5, Appli
33	487	7.5	1837	4	US-09-588-995A-5	Sequence 5, Appli
34	477	7.3	827	4	US-09-248-796A-17307	Sequence 17307, A
35	468.5	7.2	862	1	US-08-325-267A-4	Sequence 16703, A
36	449.5	6.9	529	4	US-09-248-796A-16703	Sequence 16703, A
37	441	6.8	1187	4	US-09-949-016-6513	Sequence 6513, Ap
38	440.5	6.8	2169	4	US-09-949-016-6930	Sequence 6930, Ap
39	433.5	6.7	2736	4	US-09-252-991A-30227	Sequence 30227, A
40	415.5	6.4	1306	4	US-09-538-092-330	Sequence 330, App
41	407.5	6.3	1938	4	US-09-949-016-6609	Sequence 6609, Ap
42	404.5	6.2	2035	1	US-08-046-585-5	Sequence 5, Appli
43	404.5	6.2	2035	1	US-08-393-703-5	Sequence 5, Appli
44	404.5	6.2	2035	5	PCT-US93-11721-5	Sequence 5, Appli
45	404	6.2	1747	4	US-09-134-000C-5999	Sequence 5999, Ap

ALIGNMENTS

RESULT 1

US-09-248-796A-16243
; Sequence 16243, Application US/09248796A
; Patent No. 6747137

; GENERAL INFORMATION:
; APPLICANT: Kelch Weinstein et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 16243

; LENGTH: 1191

; TYPE: PRT

; ORGANISM: Candida albicans

US-09-248-796A-16243

Query Match 64.5%; Score 4190.5; DB 4; Length 1191;

Best Local Similarity 68.1%; Pred. No. 1.2e-230; Indels 121; Gaps 19;
Matches 863; Conservative 89; Mismatches 195;

Qy	1	MLQOFTLLFLYLSTASAKTITGVFDSFNSLTWSNAANYAFKPGYPTWNAVLGWSLDCGS	60
Db	3	MLQOFTLLFLYLSTASAKTITGVFDSFNSLTWSNAANYAFKPGYPTWNAVLGWSLDCGS	62
Qy	61	ANPGDTFLNMPVCVKYTTTSQTSVDLADGVKYATCFYSGEBFTTSTLTCTVNDALKS	120
Db	63	ANPGDTFLNMPCVFRVTTTSQTSVDLADGVKYATCFYSGEBFTTSTLTCTVNDALKS	122
Qy	121	SIKAFGTWTLPIAFNVGTSSTOLEDSKCTAGTNTVTENDGDKDISIDVEFEKSTVDP	180
Db	123	SIKAFGTWTLPIAFNVGTSSTOLEDSKCTAGTNTVTENDGDKDISIDVEFEKSTVDP	182
Qy	181	SAYLYASRVMPSLNKNVTLFVAPQCENGYTSGMTGFSSNGDVAIDCSNIHIGITKGLND	240
Db	183	SGYLYASRVMPSLNKNVTLFVAPQCENGYTSGMTGFSSNGDVAIDCSNIHIGITKGLND	242
Qy	241	WNPVSVSEFSYTKTCTSNIGIQKYQNPAGYRPFIDAYISATDVNQVTLAYTNDYTCAG	300
Db	243	WNPVSVSEFSYTKTCTSNIGIQKYQNPAGYRPFIDAYISATDVNQVTLAYTNDYTCAG	302
Qy	301	SRLOSKPFTLWTKYKNSDAGSNGIVIVATRTTDSVTATVTLPPNSVDKTKTIELQ	360
Db	303	SRLOSKPFTLWTKYKNSDAGSNGIVIVATRTTDSVTATVTLPPNSVDKTKTIELQ	362

QY 944 SSVTSLTOLSIIPS-----VSESESKVFTSNGDNQSGTHDSQSTS-----TEIEIV--- 990
Db 828 QSYATTTTITVAPPGTDTVIIRPPNYVTTYEWSQSYATTTVITAPPGTDTVIIRREP 887
QY 991 ---TTSSTKVLPPVSSNLTDLTSEPTNT-----REQPT-TLSTT---SNSITEDITTSQP 1038
Db 888 PNYVTTYEWSQSYATTTTITVAPPGTATVIIRPPNYVTTYEWSQSYATTTTITGTP 947
QY 1039 TGDNGDNTSSNPVPTVATISLASASEEDNKGSHESASTSLKPSMGENSEGLTST----- 1094
Db 948 PGSTDTVIIRPPNPVTVT-----EYWSQSYATTTTITVAPPG-----TATVIIR 993
QY 1095 EIEATTTPTRAPSPAVSSGTDVTTER--TDT---REQPTLSTTSKTNSELVATQATN 1149
Db 994 EPPNTVTTYEWSQSYATTTTITGPPGDTVIIRPPNPVTTYEWS--LSYTRUSS 1051
QY 1150 ENGKKS 1155
Db 1052 ANAGRS 1057

RESULT 3
US-09-248-796A-16702
; Sequence 16702, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16702
; TYPE: PRT
; ORGANISM: Candida albicans
; NAME/KEY: UNSURE
; LOCATION: (493)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno
US-09-248-796A-16702

Query Match 42.8%; Score 2779; DB 4; Length 780;
Best Local Similarity 64.0%; Pred. No. 1.8e-150;
Matches 550; Conservative 89; Mismatches 124; Indels 96; Gaps 8;
QY 1 MQQFTLLFLYLISASAKTITGVFDSFNSLTWSNAANYAFKPGGYPTWNAVGLWSLDGTS 60
Db 3 MQQFTLLFLYLISAFATAKAITGIFNSIDLSLTWSNAGNAYFKPGGYPTWNAVGLWSLDGTS 62
QY 61 ANPGDTPLNMPGVKYYTSQTSVDLTADGVKYATCOFYSGSEPTTFSTLCTVNDALKS 120
Db 63 ANPGDTFILNMPGVKFTASOKSVDLTADGVKYATCOFYSGSEPTTFSSLKCTVNNLRS 122
QY 121 SIKAFGTVTLPAFNVGGTSDLEDSKCFAGTNTVTFNDGDKDISIDVFEKSTVDP 180
Db 123 SIKALGTVTLPAFNVGGTSSVDLEDSKCFAGTNTVTFNDGSKLSIANNFELSTWDO 182
QY 181 SAYLYASRYMPSLNKVTTLFVAPQCENGYTSCTMGFSSNGDVAIDCSNIHIGITKGLND 240
Db 183 SGVLTTRPMPSLNKIATLYVAPQCENGYTSCTMGFSTSGDVAIDCSNVHIGISGVND 242
QY 241 WNPVSSSEFSYTKTCSNGIQIKYQNVAGRPFI DAYISATDVOYTLATYNDYTCAG 300
Db 243 WNPVTSSEFSYTKCSNGISGIIYQNVAGRPFI DAYISPSDNNQYQLSKYNDYTCV 302
QY 301 SRLQSKPFTLRWTGYKNSDAGSNGIVVATTTTVDSTTAVTTLFPNPSVDKTKTIEILQ 360

Db 303 DYMQHAPFTLRWTGYKNSDAGSNGIVVATTTTVDSTTAVTTLFPNPSVDKTKTIEILQ 362
QY 361 PIPPTTTTTSVGVTTSYLAKTAPIGETATVVDVPHYHTTTTWTSEWGTITTTTTRNP 420
Db 363 PIPPTTTTTSVGVTTSYLAKTAPIGETATVVDVPHYHTTTTWTSEWGTITTTTTRNP 422
QY 421 TDSIDTIVVQVPLPNPVTSTTEYWSQSFAATTTTITVAPPGGTDTVIIRPPNHTVTTTSEW 480
Db 423 NDSIDTIVVQVPLNPITTTITQFWSSESFISITTTITNSLKGTDVIVREPHNPVTVTTSF 482
QY 481 SQSFATTTTITVAPPGGTDVUIIRPPNPVTTYEWSQSFAATTTTITVAPPGGTDVUIRE 540
Db 483 SESYATTTITXGTLGTDVUIIRPPNPVTTYEWSQSFAATTTTITVAPPGGTDVUIRE 542
QY 541 PPNPVTTYEWSQSFAATTTTITVAPPGGTDVUIIRPPNPVTTYEWSQSFAATTTTITV 600
Db 543 PHNPVTTYEWSQSFAATTTTITVAPPGGTDVUIIRPPNPVTTYEWSQSFAATTTTITV 602
QY 601 PPGGTDVUIIRPPNPVTTYEWSQSFAATTTTITVAPPGGTDVUIIRPPNPVTTYEWS 660
Db 603 KPGGTDVUIIRPPNPVTTYEWSQSFAATTTTITVAPPGGTDVUIIRPPNPVTTYEWS 651
QY 661 SQSYATTTTITVAPPGGTDVUIIRPPNPVTTYEWSQSFAATTTTITVAPPGGTDVUIR 719
Db 652 LEELSSTTAI-----ESSDSNISSAQESSSLVEQSSSIVGLSSSDIPLSS 698
QY 720 EPPNHTVTTTYEWSQSFAATTTTITVAPPGGTDVUIIRPPNPVTTYEWSQSFAATTTT 779
Db 699 DMPSSST-----GLTSS----- 712
QY 780 APPGDTTVIIEYSSMSKISTSSNDITSIIPSPRPHYVNSTSDLSSTPSSSMNTPTS 839
Db 713 -----SSTVSSYSDSS-----SSELSSTSSSESYSSISDITTFWDSS----- 752
QY 840 ISSDGLLSSTTLVTESET 858
Db 753 -SSD-----LESTLITWSSS 766

RESULT 4
US-09-248-796A-16701
; Sequence 16701, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBIC
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16701
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16701

Query Match 35.4%; Score 2297; DB 4; Length 646;
Best Local Similarity 69.0%; Pred. No. 4.2e-123;
Matches 428; Conservative 81; Mismatches 109; Indels 2; Gaps 1;
QY 8 LFLYLISASAKTITGVFDSFNSLTWSNAANYAFKPGGYPTWNAVGLWSLDGTSANPGDTF 67
Db 27 LFFYCTIAMAKTISGVFTSFNSLTWNTGNTGYGPGGYPTWNAVGLWSLDGTLASPGDTF 86
QY 68 TLNMPGVKYYTSQTSVDLTADGVKYATCOFYSGSEPTTFSTLCTVNDALKSSIKARGT 127
Db 87 TLNMPGVKYYTSQTSVDLTADGVKYATCOFYSGSEPTTFSTLCTVNDALKSSIKARGT 146

;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
;; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

;; FILE REFERENCE: 107196.132
;; CURRENT APPLICATION NUMBER: US/09/248,796A

;; PRIOR FILING DATE: 1999-02-12

;; PRIOR APPLICATION NUMBER: US 60/074,725

;; PRIOR FILING DATE: 1998-02-13

;; PRIOR APPLICATION NUMBER: US 60/096,409

;; PRIOR FILING DATE: 1998-08-13

;; NUMBER OF SEQ ID NOS: 28208

;; SEQ ID NO 14118

;; LENGTH: 501

;; TYPE: PRT

;; ORGANISM: Candida albicans

;; US-09-248-796A-14118

Query Match 23.1%; Score 1500.5; DB 4; Length 501;

Best Local Similarity 55.8%; Pred. No. 7.4e-78;

Matches 298; Conservative 84; Mismatches 91; Indels 61; Gaps 7;

Qy 396 PYHTTTTSEWTCGTTTTTTRNPTDSIDTVVQVPLPNTVSTTTEYWSQSFAITTTVT 455

Db 1 PYDPTVTTFWSESPASTTTVTNPPDGINSVIMPEY-NPTVTTFWSEFAITTTVT 59

Qy 456 APGCGTDVIREPPNHTVTTTEYWSQSFAITTTVTAPPDGTDSVIREPPNPTVTTFEY 515

Db 60 NPPDGRNSVIMPEYNTVTFEWSFAITTTVTNPPDGTNSVIMPEYNTVTFEY 119

Qy 516 WSQSFAITTTVTAPPDGTDSVIREPPNPTVTTFEYWSQSFAITTTVTAPPDGTDSVIR 575

Db 120 WSESPASTTTVTNPPDGINSVIMPEYNTVTFEWSFAITTTVTNPPDGTNSVIMK 179

Qy 576 EPPNHTVTTTEYWSQSFAITTTVTAPPDGTDSVIREPPNHTVTTTEYWSQSFAITTTVT 635

Db 180 EYPNPTVTTFEWSFAITTTVTNPPDGTNSVIMPEYNTVTFEWSFAITTTVT 239

Qy 636 GPPGTDVIREPPNPTVTTFEYWSQSFAITTTVTAPPDGTDSVIREPPNHTVTTTEY 695

Db 240 NPPDGTNSVIMPEYNTVTFEWSFAITTTVTNPPDGTNSVIMPEYNTVTFEY 299

Qy 696 WSQSFAITTTVTAPPDGTDSVIREPPNHTVTTTEYWSQSFAITTTVTAPPDGTDSVIR 755

Db 300 WSESPASTTTVTNPPDGINSVIMPEYNTVTFEWSFAITTTVTNPPDGTNSVIMK 359

Qy 756 EPPNPTVTTFEYWSQSFAITTTVTAPPDGTDSVIREPPNHTVTTTEYWSQSFAITTTVT 813

Db 360 EYPNPTVTTFEWSFAITTTVTNPPDGTNSVIMPEYNTVTFEWSFAITTTVT 419

Qy 814 -----SRPHVNSTSDLSSTFSSSMNTPTSISDGMLLSSTLVTESETTTELI 863

Db 420 SSFESTIHSSEPHY-----SSDPDS-----DSFVLISVTASSYDESS- 461

Qy 864 CSDGKCSRLSSSGIVTNPDSNESSIVTSTVPT-----ASTMSDSLSTDGISA 913

Db 462 -----IVSSFTPTLHLSSTYTWSSGLGSTRHFA 489

RESULT 12

US-09-248-796A-16245

;; Sequence 16245, Application US/09248796A

;; Patent No. 6747137

;; GENERAL INFORMATION:

;; APPLICANT: Keith Weinstock et al

;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
;; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

;; FILE REFERENCE: 107196.132

;; CURRENT APPLICATION NUMBER: US/09/248,796A

;; PRIOR FILING DATE: 1999-02-12

;; PRIOR APPLICATION NUMBER: US 60/074,725

;; PRIOR FILING DATE: 1998-02-13

;; PRIOR APPLICATION NUMBER: US 60/096,409

;; PRIOR FILING DATE: 1998-08-13

;; NUMBER OF SEQ ID NOS: 28208

;; SEQ ID NO 16245

;; LENGTH: 300

;; TYPE: PRT

;; ORGANISM: Candida albicans

;; FEATURE:

;; NAME/KEY: UNSURE

;; LOCATION: (289)

;; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unk

;; US-09-248-796A-16245

Query Match

Best Local Similarity 80.9%; Pred. No. 2.1e-61; Length 300;

Matches 228; Conservative 15; Mismatches 38; Indels 1; Gaps 1;

Qy 193 LNKVTTLFVAPQCENGYTGTCMGFSSNGSDVAIDCSNIHIGITKGLNDMNPVSSSFSY 252

Db 8 LTKQSLMWQPCANGYTGTCMGFIVLTGDTTDCSNVHVGITKGLNDMNPVSSDLSY 67

Qy 253 TKTCTSGNGIOIKYONYPAGYRPFIDAYISATDVQVTLAYTNDYTCAGSLQSKPFTLRW 312

Db 68 NKTCSSTGISITTEMFPAGYRPFDDVTVLSDQNR-QLKYTNDYACVSSLSQSKPFLRL 126

Qy 313 TGYKNDAGSNGIVVATRTTVDSTTATVTLBNPSVDKTKTIELLOPIPTTTITSYV 372

Db 127 RGYNNSEANSNGFVAVATRTTVDSTTATVTLBNPSVDKTKTIELLOPIPTTTITSYV 186

Qy 373 GVTTSYLTKTAPIGETATVVDVPHYTTTTSVSEWGTITTTTTRNPTDSIDTVVQVP 432

Db 187 GVSTSYLTKTAPIGETATVVDVPHYTTTTSVSEWGTITTTTTRNPTDSIDTVVQVP 246

Qy 433 LPNPTVTSTTEYWSQSFAITTTVTAPPDGTDSVIREPPNHTV 474

Db 247 LPNPTVTSTTEYWSQSFAITTTTAHPDGTDSVIREPPNHTV 288

RESULT 13

US-09-248-796A-14117

;; Sequence 14117, Application US/09248796A

;; Patent No. 6747137

;; GENERAL INFORMATION:

;; APPLICANT: Keith Weinstock et al

;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
;; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

;; FILE REFERENCE: 107196.132

;; CURRENT APPLICATION NUMBER: US/09/248,796A

;; CURRENT FILING DATE: 1999-02-12

;; PRIOR APPLICATION NUMBER: US 60/074,725

;; PRIOR FILING DATE: 1998-02-13

;; PRIOR APPLICATION NUMBER: US 60/096,409

;; PRIOR FILING DATE: 1998-08-13

;; NUMBER OF SEQ ID NOS: 28208

;; SEQ ID NO 14117

;; LENGTH: 240

;; TYPE: PRT

;; ORGANISM: Candida albicans

;; US-09-248-796A-14117

Query Match

Best Local Similarity 96.7%; Pred. No. 1.2e-57; Length 240;

Matches 231; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1027 NSITEDITTSQPTGNDGNDTSSNTPVPTVATSTLASAEDNKGSHESASTSLKPSMGE 1086

Db 7 NPSREDITTSQPTGNDGNDTSSNTPVPTVATSTLASAEDNKGSHESASTSLKPSMGE 66

Qy 1087 NSGLTSTTEIATTTSTPEAPSPAVSGTDTTPTTRETQPTTLSTTKNSSELVATQ 1146

Db 67 NSGLTSTTEIATTTSTPEAPSPAVSGTDTTPTTRETQPTTLSTTKNSSELVATQ 126

Qy 1147 ATNENGKSPSTDLTSSLTGTSASTSANGSELVSGSVTGAVASANDQSHSVTSNSN 1206

Db 127 ATNENGKSPSTDLTSSLTGTSASTSANGSELVSGSVTGAVASANDQSHSVTSNSN 186

QY 1207 SIVSNTPTQTLSQOVTSSSPTNTFFIASTYDGSIIHQHSTWLYGLITLISLFI 1260
Db 187 SIVSNTPTQTLSQOVTSSSPTNTFFIASTYDGSIIHQHSTWLYGLITLISLFI 240

RESULT 14

US-08-325-267A-2
; Sequence 2, Application US/08325267A
; Patent No. 5585271
; GENERAL INFORMATION:
; APPLICANT: WATARI, JUNJI
; APPLICANT: TAKATA, YOSHIHIRO
; APPLICANT: OGAWA, MASAHIRO
; APPLICANT: PENTTILA, MERJA
; APPLICANT: ONNELA, MAIJA-LEENA
; APPLICANT: KERANEN, SIRKKA
; TITLE OF INVENTION: YEAST AGGLUTINATION GENES AND YEAST
; TITLE OF INVENTION: CONTAINING THEM
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HWY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,267A
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP PCT/JP94/00290
; FILING DATE: 24-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 38871/1993
; FILING DATE: 26-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/POCKET NUMBER: 2589-023-0XPCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1537 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-325-267A-2

Query Match 14.5%; Score 940; DB 1; Length 1537;
Best Local Similarity 26.0%; Pred. No. 3e-45;
Matches 417; Conservative 244; Mismatches 523; Indels 418; Gaps 85;

QY 2 LQQFTLLFLYLISASAKT-----ITGVFDSF-----NSLTWSNAANYAF----- 40
Db 10 LAVFTLLAL-TSVASGATEACLPAGQRKSGMNINFYQYSLKDSSTYSNAAVMAYGYASKT 68
QY 41 -----KQGGYPTW-----NAVLGWSLD--G 58
Db 69 KLGSVGGQTOISIDYNIPCVSSSGTFPCQPDSDSYGNMGCKGMGACNSQGIAYWSTDLFG 128
QY 59 TSANPGDTFTLNM-----PCVFKYTTSQ-----TSVD 85
Db 129 FYTFTTNV-TLEMTGYFLPPQTGTYTFKATVDDSAILSVGGATAFNCCAQOQPPITSTN 187

QY 86 LTADGVK-----YACQFYSGEEFTTFTSTLTCTVNDALKSIIKAFGT-----VTLP 131
Db 188 FTIDGIKPWGSGSLPPNIEGTVMYAGYYPM-----KVYSNAVSGWGLPISVITLP 238
QY 132 IAFNVGCTSSDLEDSKCFAGTNTVTFNDGDKOISIDVEFEKSTV-DPSAYLYASRV 190
Db 239 -----DGTTVSDDFEG-----YVYSFDD-----DLQSQNCVTPDPSNVA-VSTTT 277
QY 191 PSLNKVTTILFVAPQCENGYSCTMGFSSSGNDGVAIDCSNIHIGITKGLDNWNPVSESF 250
Db 278 TTTEPWTGFTSTSTEMTIVTGNGVPTDETVIVIRPTTASTIIITTEPWNSTFTST 337
QY 251 SYTKTCTNSGIIQKQNPAGYRPFIDAYISATDVNQYTLAYNDVTCAGSRLOKRPFL 310
Db 338 ELTTVTGNGVRDETI-----VIRPTTATTATTTEPWNSTFTSTSTEL----- 384
QY 311 RWTGYNKSDAGNGI---VIVATTRVTDSTTAVTL-PPNPSVDTKI----- 355
Db 385 -----TTVTGNGLPFDETIIVIRPTTATTAMTTQPNNDTFTSTSTEMTIVTGNGL 438
QY 356 -----IEILOPIPTTTIIT-----SYGVVTSYLTAKTA-----PIGETATVIVDVPYH 398
Db 439 PTDETIIVIRPTTATTAMTTQPNNDTFTSTSTEMTIVTGNGLPFDETI-IVIRPTT 497
QY 399 TTT--TVTSEWTGTT-----TTTTRN--PTDSIDTVVQVPLNPPT-VSTTEYWSQS 447
Db 498 ATTAMTTQPNNDTFTSTSTEMTIVTGNGLPFDETI-IVIRPTTATTAMTTQPNNDT 556
QY 448 FATT-----TTVTAPPG-GTD--TVIIREPPNHT--VTTTEYWSQSFAIT-----TTVTAPP 494
Db 557 FTSTSTEMTIVTGNGLPFDETIIVIRPTTATTATTTEPWNSTFTSTSTELTIVTG 616
QY 495 G-GTDS--VIREPPNPT--VTTTEYWSQSFAIT-----TTVTAPPG-GTDS--VIREPP 542
Db 617 GLPTDETIIVIRPTTATTAMTTQPNNDTFTSTSTEMTIVTGNGLPFDETIIVIRPT 676
QY 543 NPT--VTTTEYWSQSFAIT-----TTVTAPPG-GTDS--VIREPPNHT--VTTTEYWSQS 591
Db 677 TATTAMTTQPNNDTFTSTSTEMTIVTGNGLPFDETIIVIRPTTATTAMTTQPNNDT 736
QY 592 YATT-----TTVTAPPG-GTD--TVIIREPPNHTV--TTTEYWSQSFAIT-----TTVT 635
Db 737 FTSTSTEMTIVTGNGVPFDETVIVIRPTSEGLISTTTEPWTGFTSTSTEMTIVTG 796
QY 636 GPPSGTDTVIREPPNP--TVITTEYWSQSFAIT-----TTITAP--PGSTDVLIAREPP 696
Db 797 GQPTDETVIVIRPTSEGLVTTTTEPWTGFTSTSTEMTIVTGNGVPFDETVIVIRPT 856
QY 687 NHTV--TTTEYWSQSFAIT-----TTVTAPPG-GTD--TVIIREPPNHTV--TTTEYWSQS 735
Db 857 SEGLISTTTEPWTGFTSTSTEMTIVTGNGQPTDETVIVIRPTSEGLISTTTEPWTGT 916
QY 736 YATT-----TTVTAPPG-GTD--TVIIREPPNHTV--TTTEYWSQSFAITTTVTAPP 785
Db 917 FTSTSTEMTIVTGNGVPFDETVIVIRPTSEGLISTTTEPWTGFTSTSTEMTIVTG 976
QY 786 -----DTVIIYESMSSSKI-----STSSNDITSIIIPFSRP----- 816
Db 977 GQPTDETVIVIRPTSEGLISTTTEPWTGFTSTSTEMTIVTGNGQPTDETVIVIRPT 1036
QY 817 --HYVNSTTSD-LSITFESSNMPTSISSDGMLLSSTLVTESETT-----TELICDGKE 869
Db 1037 SEGLVTTTTEPWTGFTSTSTEMTIVTGNGLPFDETVIVIRPTTATSSLSSSSGQI 1096
QY 870 CSRLLSSSGGVTPN--DSNESSIVTGTPTASTMDSLSLSDGISATSSDNVSKSGSV 927
Db 1097 TSSITSSRPIT--PFPNSNGTSVSSSVSSVSSVSSVSSVSSVSSVSSVSSVSSVSS 1155
QY 928 TETSVTTIQTNPPLSSSVTSLTQLSIPSVSSESKVFTFSGNDGNQSGTHDSQSTSEI 987
Db 1156 SSSKSSV--IPTSSSTSGSSESTSGAGVSSS-----SPISSESSKSPYSSSS--L 1205
QY 988 EIVTTSST-----KVLPPVSSNVDLTSEPTNREQPTLSTTS-----NSITEDITT 1035

Db	1206	PLVTSATTSQETASSLPATT-----TKTSEQTLTVTSCESHVCTESISPAIVS	1256
Qy	1036	SQPTGDNQDNTSSN--PVPTVAISTLASAEHKNKSGSHESASTSLKPSMGENGSLTTS	1093
Db	1257	TATVTVSGVTEYTTWCPISTTETTKQTGTEQTTETTKQTTVTTISSCESDVCSTAS	1316
Qy	1094	TEIRATTTSPTEAPSPAVSSGTDVTRPTDRQOPTLSTT-----SKTNSLVATT-	1145
Db	1317	PAIVSTSTATINGVTTEYTTWCPIST--TESRQQTLLVTVTSCSGVCSETASPAIVSTA	1374
Qy	1146	-----QATNENGKGSPTDLTSSLTTGT-SASTSANSSELVTSQVTTGGA	1188
Db	1375	TATVNDVVVYPTWRPQTANESVSSKMSATGETTTNLAAETTTNTVAAETITNTGAA	1434
Qy	1189	-----VASANDQSHSTSV-----TNSNSIVSNTPQTLLSQQVTS	1224
Db	1435	ETKTVTSSLSRSHAEQTASATDVIGHSSSVSVSETGNTKSLTSSGLSTMNQPRST	1494
Qy	1225	SP-----STNTFIASIVDGGSSIIQHSHTWLYGLITLLSLFI	1260
Db	1495	PASSVMGVSTASLEISTTAGSANSLLAGSLSVFIASLLLA	1536

RESULT 15

US-09-248-796A-16698

; Sequence 16698, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR FILING DATE: 1999-02-12

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 16698

; LENGTH: 229

; TYPE: PRT

; ORGANISM: Candida albicans

US-09-248-796A-16698

Query Match

Best Local Similarity

Matches 153; Conservative 22; Mismatches 27; Indels 0; Gaps 0;

12.5%; Score 815; DB 4; Length 229;

75.7%; Pred. No. 3e-39;

Qy	1	MLQQFTLLFLYLSTIASAKTITGVFDSFNSLTWSNANYAFKPGYPTWNAVLGWSLDGTS	60
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Qy	61	ANPGDFTLNMPGVKFTYTSQTSVDLTADGVKATCFQVSGEFTTPTSTLTCTVNDALKS	120
Db	69	ANPGDFTLNMPGVKFTYTDQTSVDLTAGVKIATCFQVSGEFTTPTSTLTCTVNDALKS	128
Qy	121	SIKAFGTVTLPIAFNVGGTGSSTDLSDSKCFKCTAGTNTVTFNDGDKDIDIVFEFKSTVDP	180
Db	129	SIKALGTVTLPIAFNVGGTGSSTDLSDSKCFKCTAGTNTVTFNDGDKKISIDVDPEKTNEDA	188
Qy	181	SAYLASRVMPSLNKVTTLFVA	202
Db	189	SGYFIASRLIPSINKASITYVA	210

Search completed: September 8, 2005, 18:28:14
Job time : 51 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: September 8, 2005, 18:26:58 ; Search time 184 Seconds
(without alignment)
2696.833 Million cell updates/sec

Title: US-09-715-876-8
Perfect score: 6495
Sequence: 1 MLOQFTLLFLYLSTASAKTI.....SIQHSTWLYGLITLLSLFI 1260

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1774312 seqs, 393823214 residues 1774312
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	6465	99.5	1260	14	US-10-245-802-8
2	4204.5	64.7	1119	14	US-10-245-802-12
3	3938.5	60.6	1047	14	US-10-245-802-22
4	2680.5	41.3	1443	14	US-10-245-802-18
5	2584.5	39.8	1270	14	US-10-245-802-16
6	2452.5	37.8	2297	14	US-10-245-802-20
7	1992.5	30.7	468	14	US-10-245-802-10
8	1819	28.0	469	14	US-10-245-802-14
9	1717.5	26.4	468	14	US-10-245-802-24
10	939	14.5	1537	9	US-09-801-368-104
11	939	14.5	1537	15	US-10-369-493-1398

12	939	14.5	1537	17	US-10-324-035-17	Sequence 17, Appl
13	932.5	14.4	1322	9	US-09-801-368-114	Sequence 114, App
14	932.5	14.4	1322	15	US-10-369-493-1353	Sequence 1353, Ap
15	721.5	11.1	5179	9	US-09-922-217-1068	Sequence 1068, Ap
16	721.5	11.1	5179	9	US-09-833-263-1068	Sequence 1068, Ap
17	721.5	11.1	5179	13	US-10-025-380-1068	Sequence 1068, Ap
18	721.5	11.1	5179	16	US-10-734-564-121	Sequence 121, App
19	711	10.9	1075	9	US-09-801-368-110	Sequence 110, App
20	711	10.9	1075	15	US-10-369-493-22068	Sequence 22068, A
21	675.5	10.4	1367	9	US-09-801-368-108	Sequence 108, App
22	658	10.1	1831	15	US-10-282-122A-71033	Sequence 71033, A
23	658	10.1	1870	17	US-10-470-048B-268	Sequence 268, App
24	657.5	10.1	4262	17	US-10-704-781-4	Sequence 4, Appll
25	657.5	10.1	4493	17	US-10-704-781-3	Sequence 3, Appll
26	651	10.0	2137	18	US-10-724-972A-4951	Sequence 4951, Ap
27	646.5	10.0	2283	14	US-10-172-502-4	Sequence 4, Appll
28	646.5	10.0	2283	19	US-11-020-509-4	Sequence 4, Appll
29	640.5	9.9	2261	17	US-10-470-048B-60	Sequence 60, Appl
30	640.5	9.9	2344	9	US-09-815-242-12713	Sequence 12713, A
31	637.5	9.8	2271	15	US-10-282-122A-43924	Sequence 43924, A
32	624	9.6	800	14	US-10-029-386-32198	Sequence 32198, A
33	577.5	8.9	957	10	US-09-840-746-19	Sequence 19, Appl
34	577.5	8.9	1217	16	US-10-734-564-122	Sequence 122, App
35	574	8.8	1283	15	US-10-369-493-22616	Sequence 22616, A
36	553.5	8.5	1459	15	US-10-369-493-6418	Sequence 6418, Ap
37	547.5	8.4	1609	15	US-10-369-493-1535	Sequence 1535, Ap
38	545.5	8.4	957	9	US-09-922-217-1065	Sequence 1065, Ap
39	545.5	8.4	957	9	US-09-833-263-1065	Sequence 1065, Ap
40	545.5	8.4	957	13	US-10-025-380-1065	Sequence 1065, Ap
41	522.5	8.0	5877	14	US-10-142-515-11	Sequence 11, Appl
42	519.5	8.0	1794	10	US-09-965-738-299	Sequence 299, App
43	519.5	8.0	1799	10	US-09-965-738-149	Sequence 149, App
44	519.5	8.0	1821	10	US-09-965-738-82	Sequence 82, Appl
45	519.5	8.0	11721	10	US-09-965-738-162	Sequence 162, App

ALIGNMENTS

RESULT 1
US-10-245-802-8
; Sequence 8, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245.802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 8
; LENGTH: 1260
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-245-802-8

Query Match	99.5%	Score	6465;	DB	14;	Length	1260;
Best Local Similarity	99.6%	Pred. No.	0;				
Matches	1255;	Conservative	0;	Mismatches	5;	Indels	0;
Gaps	0;						
Qy	1	MLOQFTLLFLYLSTASAKTI	GVDFDSFNSLTWSNAANYAFKPGYPTWNAVGLWSLDGTS	60			
Db	1	MLOQFTLLFLYLSTASAKTI	GVDFDSFNSLTWSNAANYAFKPGYPTWNAVGLWSLDGTS	60			
Qy	61	ANPGDTFTLNMPCKVFKYTT	QTSVDLTADGVKYATCQFYSGBEFTTFTGTLCTVNDALKS	120			
Db	61	ANPGDTFTLNMPCKVFKYTT	QTSVDLTADGVKYATCQFYSGBEFTTFTGTLCTVNDALKS	120			
Qy	121	SIKAFGTVTLPIAFNVG	TGSGSTDLDSKCFAGTNTVTTFNDGDKDISIDVEFEKSTVDP	180			

Db 121 SRAFGVTLPAPFVGGTSSDLEDSKCFAGTNTVTFNDGDKDISIDVPEKSTVDP 180
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Db 181 SAYLYASRVMPSLNKVTTLVFAPQCENGYTSGTMGSSNGDVADICSNHIGITKGLND 240
QY 241 WNPVSESPSYTKTCTSNIGIQIKYQNVAPAGYPPFDAYISATDVNQYTLAYTNDYTCAG 300
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Db 301 SRLQSKPFTLRWTKYKNSDAGSNGIVATRTVTDSTTAVTLPFPNPSVDKTKTIELQ 360
QY 361 PIPPTTTTTSYGVGVTTSYLTAKTAPIGETATVVDVPHHTTTTSEWTKTITTTTTRNP 420
Db 361 PIPPTTTTTSYGVGVTTSYLTAKTAPIGETATVVDVPHHTTTTSEWTKTITTTTTRNP 420
QY 421 TDSIDTVVQVPLPNPTVSTTEYWSQSFATTTTVPAGGTDVTVIIRPPNHTVTTTEY 480
Db 421 TDSIDTVVQVPLPNPTVSTTEYWSQSFATTTTVPAGGTDVTVIIRPPNHTVTTTEY 480
QY 481 SQSFATTTTVPAGGTDVTVIIRPPNHTVTTTEYWSQSFATTTTVPAGGTDVTVIIR 540
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Db 541 PPNPTVTTTEYWSQSYATTTTVPAGGTDVTVIIRPPNHTVTTTEYWSQSYATTTT 600
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QY 841 SSDGMLLSSTPLVTESETTTBELICSDGKCSRLLSSSGIVTNPDNNESSIVTSTVPTAST 900
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QY 901 MSDLSSTDGLSATSSDNVSKSGVSTETSVTTIQTTPNPLSSSVTLQLSSIPVSE 960
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Db 1141 SVATTQATNENGKSPSTDLTSSLTGTSTASSELVTSVSGVGTGAVASANDQSHST 1200
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Db 1201 SVTNSNGIVSNTPQTTLSSQVTSSTSPNTFIATYDGSIIQHSWTWLYGLITLLSLFI 1260
RESULT 2
US-10-245-802-12
; Sequence 12, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 12
; LENGTH: 1119
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-245-802-12
Query Match 64.7%; Score 4204.5; DB 14; Length 1119;
Best Local Similarity 64.9%; Pred. No. 1.7e-207;
Matches 844; Conservative 106; Mismatches 128; Indels 223; Gaps 18;
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Db 181 SAYLYASRVMPSLNKVTTLVFAPQCENGYTSGTMGSSNGDVADICSNHIGITKGLND 240
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Db 721 PPNHTVTTTEYWSQYATTTTATPPGDTVLIREPPNHHVTTTTEYWSQSFAATTTTATPPGDTVLIRE 780
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Qy 865 SDGKECRLSSSGIVTPDNESIVTSVPTASTMSDLSSTDGISATSSDNVSKGV 924
Db 867 EGDGCSWVSSTRIVTPNNIETPMVNTVDSTTETS-QSPSGI-----FSESgv 918
Qy 925 SVTTETS-VTTIQTTPNPLSSVTSLTQLSSIPVSESESKVFTPSNGDNQSGTHDSQST 983
Db 919 SVETESSVTTAQTN-----PSVPTTESEVWTTKGNMENGPEPST 961
Qy 984 STEIEIVTTSKVLPPVVSNTDLTSEPTNTRQPTTLSTTSNSITEDITTSOPTDNG 1043
Db 962 N-----VKSSMDENSEFT----- 974
Qy 1044 DNTSSTNPVPTVATSLASAEEDKSGSHESASTSLKPSMGENSEGLTSTEIE---ATT 1100
Db 975 -----TSTAAS-----TSTDIENTIAT 992
Qy 1101 TSPTREAPVAVSGGDTVTTEPTDTRQPTTLSTTSKTNSELVATTOATNEN-GGKSPSTD 1159
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Db 1081 QMTSSLVSLH--MLTTPDGSVIOHSTWLCGLITLLSLFI 1119

RESULT 3
US-10-245-802-22
; Sequence 22, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; FILE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 1047
; TYPE: PR1
; ORGANISM: Candida albicans
US-10-245-802-22

Query Match 60.6%; Score 3938.5; DB 14; Length 1047;
Best Local Similarity 63.7%; Pred. No. 7.2e-194;
Matches 806; Conservative 116; Mismatches 120; Indels 223; Gaps 18;
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Db 1 MLQQTFLLLLYLSVATAKTIITGVDFSNLSLWNSNAANYHYKPGPYPTNAVLGWSLDGTS 60

Qy 61 ANPGDTFTLNPVCVKYKTTSTQTSVDLTADGVKATCOFYSGEBFTTSTLTCTVNDALKS 120
Db 61 ASPGDTFTLNPVCVKFTTSTQTSVDLTADGVKATCOFYSGEBFTTSTLTCTVNDALTP 120
Qy 121 SIKAPGTVTLPIAPNVTGCTSDLEDSKCTAGTNTVTFNDGDKDISIDVPEKSTVDP 180
Db 121 SIKALGTVTLPIAPNVTGCTSDLEDSKCTAGTNTVTFNDGDKDISINVDERSNDP 180
Qy 181 SAYLYASRVNMFSLNKVTTFLFVAPQCENGYTSGTMFSSNGSDVAIDCSNIHIGITKGLND 240
Db 181 KGYLTSRVNMFSLNKVTTFLFVAPQCENGYTSGTMFSSNGSDVAIDCSNIHIGITKGLND 240
Qy 241 WNPVSVSESPYTKTCTNSNGIQIKYQNPAGYRPFIDAYISATDVNQYTLAYTNDYTCAG 300
Db 241 YNPVSVSESPYTKTCTNSNGIFITYKNVPAGYRPFVDAYISATDVNGYTLISYANETCAG 300
Qy 301 SRLOSKPTLRWQYKNSDAGSNGIVATVTRVTDSTTATVTLPPNPSVDKTKTIBLQ 360
Db 301 GYYORAPFTLRYTGYRNSDAGSNGIVATVTRVTDSTTATVTLPPNPSVDKTKTIBLQ 360
Qy 361 PIPPTTTTTSVGVVTSYLTAKTAPIGETATVIVDVPYHTTITVTSEWTGTTTTTTRNP 420
Db 361 PIPPTTTTTSVGVVTSYLTAKTAPIGETATVIVDVPYHTTITVTSEWTGTTTTTTRNP 420
Qy 421 TDSIDTVVQVPLNPVSTTEYWSQSFAATTTTATPPGDTVLIREPPNHHVTTTTEYWS 480
Db 421 TDSIDTVVQVPSNPVTTTTEYWSQSFAATTTTATPPGDTVLIREPPNHHVTTTTEYWS 480
Qy 481 SOSFAATTTTATPPGDTVLIREPPNHHVTTTTEYWSQSFAATTTTATPPGDTVLIRE 540
Db 481 SESYTTTSTTATPPGDTVLIREPPNHHVTTTTEYWSQSFAATTTTATPPGDTVLIRE 540
Qy 541 PPNHTVTTTEYWSQYATTTTATPPGDTVLIREPPNHHVTTTTEYWSQSFAATTTTATPPGDTVLIRE 600
Db 541 PPNHTVTTTEYWSQYATTTTATPPGDTVLIREPPNHHVTTTTEYWSQSFAATTTTATPPGDTVLIRE 600
Qy 601 PPGGDTVLIREPPNHHVTTTTEYWSQSFAATTTTATPPGDTVLIREPPNHHVTTTTEYWS 660
Db 601 PPGGDTVLIREPPNHHVTTTTEYWSQSFAATTTTATPPGDTVLIREPPNHHVTTTTEYWS 660
Qy 661 SOSYATTTTITAPPGTDTVLIREPPNHHVTTTTEYWSQSFAATTTTATPPGDTVLIRE 720
Db 625 SOSYATTTTITAPPGTDTVLIREPPNHHVTTTTEYWSQSFAATTTTATPPGDTVLIRE 684
Qy 721 PPNHTVTTTEYWSQYATTTTATPPGDTVLIREPPNHHVTTTTEYWSQSFAATTTTATPPGDTVLIRE 780
Db 685 PPNHTVTTTEYWSQYATTTTATPPGDTVLIREPPNHHVTTTTEYWSQSFAATTTTATPPGDTVLIRE 744
Qy 781 PPGGDTVLIREPPNHHVTTTTEYWSQSFAATTTTATPPGDTVLIREPPNHHVTTTTEYWSQSFAATTTTATPPGDTVLIRE 840
Db 745 PPGGDTVLIREPPNHHVTTTTEYWSQSFAATTTTATPPGDTVLIREPPNHHVTTTTEYWSQSFAATTTTATPPGDTVLIRE 776
Qy 841 SSDGMLLSSTLVLVETSETTELICSDGKESRLSSSGIVTPDNESIVTSVPTAST 900
Db 777 -----LYSTTVIETKITETSCGDKGSYVSTRIVTPNNIETPMVNTVDSTTETS 830
Qy 901 MSDLSSTDGI SATSDNVSKGSVVTETS-VTTIQTTPNPLSSSVTSLAQLSIPSVS 959
Db 831 ESTS-QSPSGI-----FSESgvVETESTVTTAQTN-----PSPV 865
Qy 960 ESESKVFTPSNGDNQSGTHDSQSTSTEIEIVTTSKVLPPVVSNTDLTSEPTNTRQPT 1019
Db 866 TTESEVFTTKGNNGNGPYBSPSTH-----VKSSMDENSEFT----- 902
Qy 1020 TTLSTTSNITEDITTSOPTDNGDNTSSNTPVPTVATSLASAEEDKSGSHESASTS 1079
Db 903 -----TSTAAS----- 908
Qy 1080 LKPSMGENSEGLTSTEIE---ATTTSPTPEAPSVSGDTVTTEPTDTRQPTTLSTTSK 1136
Db 909 -----TSTDIENTIATGSEASPISSADET-----TITTTAE 946
Qy 1137 TNSBLVATTOATNEN-GGKSPSTDLTSSLTGTGASTSANSBLVTSVGTGAVASAND 1195

FILE REFERENCE: 013361.4003
CURRENT APPLICATION NUMBER: US/10/245,802
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: US 09/715,876
PRIOR FILING DATE: 2000-11-18
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.2
SEQ ID NO 16
LENGTH: 1270
TYPE: PRT
ORGANISM: Candida albicans
US-10-245-802-16

Query Match 39.8%; Score 2584.5; DB 14; Length 1270;
Best Local Similarity 45.0%; Pred. No. 2.8e-124;
Matches 616; Conservative 195; Mismatches 347; Indels 211; Gaps 37;

Qy 1 MLOQFTLLFLYLISASAKITGVFDSFNSLTWSNAAYAFKPGYPTWNAVLGSLDGT 60
Db 1 MIQFTLLFLYLSPATAKAITGFNSIDSLYSNAGNAYAFKPGYPTWNAVLGSLDGT 60

Qy 61 ANPGDTFLNMPGVKPYKTSQTSVDLTADGVKYATCQYSGEETFTSLTCTVNDALKS 120
Db 61 ANPGDTFLNMPGVKPYKTSQTSVDLTADGVKYATCQYSGEETFTSLTCTVNDALKS 120

Qy 121 SIKAGTGTLPFAFNVGSGSTLDESKCTAGTNTVTNDGDKDISIDVEFEKSTVDP 180
Db 121 SIKAGTGTLPFAFNVGSGSTLDESKCTAGTNTVTNDGDKDISIDVEFEKSTVDP 180

Qy 181 SAYLYASRMPSLNKVTLFVAPQCEGYTSGTMGFSSNGDVAIDCSNIHIGITGLND 240
Db 181 SGYLTTSRPFMSLNKIALTYVAPQCEGYTSGTMGFSTSYGDVAIDCSNVHIGISGVND 240

Qy 241 WNPVSSSFSYTKCTGNGIOIKQNPAGRPIDAYISATDVNQYTLAYNDYTCAG 300
Db 241 YNHPVTSESFSYTKSCSFGISITYQNPAGRPIDAYISPSDNNQYLSKYNDYTCVD 300

Qy 301 SRLQSKPTLRTWGVKNSDAGNGIVIVATRTVTDSTAVTTLPPNPSVDKTKIELQ 360
Db 301 DYQCHAPFTLKYTKVNSDAGNGIVIVATRTVTDSTAVTTLPPNPSVDKTKIELQ 360

Qy 361 PIPTTIITTSVGVVTSYLTAPIGETATVIDVPYHTTTVTSEWGTITTTTTTRNP 420
Db 361 PIPTTIITTSVGVVTSYLTAPIGETATVIDVPYHTTTVTSEWGTITTTTTTRNP 420

Qy 421 TDSIDTVVQVPLNPNTVSTTEYWSQSFATTTVTAPGGTDTVIIRPPNHTVTTEYW 480
Db 421 TDSIDTVVQVPLNPNTVSTTEYWSQSFATTTVTAPGGTDTVIIRPPNHTVTTEFY 480

Qy 481 SQSFATTTVTAPGGTDSVIIRPPNPTVTT-----EYWSQSFATTTVT 527
Db 481 SESYATTTITGPGTDSVIHDPLESSSTTALESDDNISQAQSSSVQSSSIV 540

Qy 528 APPGGTDSVIIRPPNPTVTTTEYWSQFATTTVTAPPGTDSVIIRPPNHTVTTEY 587
Db 541 GLSSSDIPLSDMPS-----SSSTGLTSSESTVSSVSDSSSSSELSFSSSES 591

Qy 598 WSQSFATTTVTAPPGTDTVIIRPPNHTVTTEYWSQFATTTVTGPGSGTDTVIIR 647
Db 592 YSSSIDSTNPF-----YDSSSDLESTSIYSSSIDAQSS----- 626

Qy 648 EPPNPTVTTTEYWSQFATTTITAPGE-----TDTVLIRPPNHTVTTEYWSQYA 701
Db 627 -----OSVQSVNSISQTSQETSSGSEENSTVTD-ILVSSDASSILNSD---ISSY 675

Qy 702 TTTTVPAGEDTVLIRPPNHTVTTEYWSQFATTTVTAPPGTDTVIIRPPNPT 761
Db 676 PSTTISLSDDPHTI-AGEPDSR-----SSSIASIVETIS-----SDLVSLSDP--- 719

Qy 762 VTTTEYWSQFATTTVTAPPGTDTVIIRPPNHTVTTEYWSQFATTTITIPFS----- 814
Db 720 --TSSPDSSSSLNSDSSSP-----PSDESIDISASSSPSTLVAPSPSLSSSSL 766

Qy 815 ---RPHVNSTSDLSSTFESSMNTPTSISSDGLMLSSLTTLVTESETTELLICSDGKE-- 869
Db 767 SLIIVPHVNSTTTHASESESSSVASP-SVASESANDDTHL-SESTDTTIIIGTSTVT 824

Qy 870 -CSRLSSSGIYV-----NPDSSNESSIVTSTVTASTMSDLSLSDGIGSATSSDNV--SK 921
Db 825 FCRDNGDGCIVTIGTSSSIDSEQTSDVTT---TSSFVASSTPTSAQSITDNFNIDSSQ 881

Qy 922 SGVSVTTTETSVTTIQTTPNPLSSSVTSLTQLSSIPSVSESESKVTFSTNGD----NOSGT 977
Db 882 TSASSSTKSSVSDVTVNSILLSET--TLSSDDGTS-SDTSSISTTNSDTCGINAGSS 938

Qy 978 HDQSQTSTREIIVTTS---STKVLPPVVSNTDLTSEPTWTR-----EOPITLSTTNS 1028
Db 939 HKSTASIKESSIOKTGVTLSSTLSTKLSSTDIETLITELTITIEDNPNFTSTPSS 998

Qy 1029 ITEDIITTSQPTGNG-----DNTSSNTPVPTVATSTLASAREDNKSGSHESASTSLKP 1082
Db 999 HSEIFSS-----DNSVLKQVDRSTIKTPTDVTIVSSLSVHST-----ASTA--- 1044

Qy 1083 SMGENS-----GLTSTREIATTTTPTTEAPSPAVSSGT-----DVTTEPTDT--- 1124
Db 1045 TLGENSFNVASTPLNTATSLRSTSSSNHATE---SSGTVKSEASVEAIPSPPTSTDNR 1101

Qy 1125 -----REOPTTLSTTSKTN-----SELVATQATN---ENGKSPSTDLTSSLTGTSA 1170
Db 1102 LSVSTEEAEGITVANSSTNNLITESQVAAAPTOSTSVLIENLVVTSTFDONSSAAVDQPS 1161

Qy 1171 STSANSRLV---TSGSVTCGAVASANDQSHSTSV-----TNSNSIVS 1210
Db 1162 KTKSIEESIMNPSTNETNNGFIATLSQAVPSSSIHSELIISTTAKTTDASMMGDSAA 1221

Qy 1211 NTPOTLTSQVTSSTNTFIASDYGSGSIIOHSTWLYGLITLLSLF 1259
Db 1222 NSQPTLLIQVATS--SYNQPLITYAGSSSATKHPSYLLAKFISVALFF 1268

RESULT 6
US-10-245-802-20
Sequence 20, Application US/10245802
Publication No. US20030124134A1
GENERAL INFORMATION:
APPLICANT: Edwards, John B.
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
FILE REFERENCE: 013361.4003
CURRENT APPLICATION NUMBER: US/10/245,802
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: US 09/715,876
PRIOR FILING DATE: 2000-11-18
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.2
SEQ ID NO 20
LENGTH: 2297
TYPE: PRT
ORGANISM: Candida albicans
US-10-245-802-20

Query Match 37.8%; Score 2452.5; DB 14; Length 2297;
Best Local Similarity 40.3%; Pred. No. 3.3e-117;
Matches 581; Conservative 234; Mismatches 416; Indels 211; Gaps 24;

Qy 2 LQOFTLLFLYLISAS--AKTITGVFDSFNSLTWSNAAYAFKPGYPTWNAVLGSLDGT 59
Db 1 MKKLYLLYLASFTTVISKEVGVFNQFNSLIYSYTRARYEEISTLTANAQLEVALDGT 60

Qy 60 SANPGDTFLNMPGVKPYKTSQTSVDLTADGVKYATCQYSGEETFTSLTCTVNDALK 119
Db 61 IASPGDTFLNMPGVKPYKFTVETSVQLTANSIATCFDAGEDTKPSLSLCTVDELT 120

Qy 120 SSIKAGTGTLPFAFNVGSGSTLDESKCTAGTNTVTNDGDKDISIDVEFEKSTVD 179
Db 121 EDTSVFSGVILPIAFNVGSGSKSTITDSKCFSSGYNTVTFDGNQNLSTTANFLPREL 180


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RESULT 8
US-10-245-802-14
; Sequence 14, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-245-802-14

Query Match      28.0%; Score 1819; DB 14; Length 469;
Best Local Similarity 72.1%; Pred. No. 1.7e-85;
Matches 338; Conservative 48; Mismatches 83; Indels 0; Gaps 0;

Qy 1 MLOQFTLLFLYLISAKTIITGVDFNSLTSNAANYAFKPGYPTWNAVLSLGDTS 60
Db 1 MLLQFLLSLCVATKIVTGVSFNSLTSNAANYAFKPGYPTWNAVLSLGDAT 60
Qy 61 ANPGDTFTLNMPCVKYTTTSOTSDLTADGVKATCQFYSGERTFTSLTCTVNDALKS 120
Db 61 ASAGDTFTLDMPCVKFKFTDQTSIDLVDAGRTYATCNLSAREFTTSSVSCVTWTWA 120
Qy 121 SIKAFGTTLPIAFNVGGTGSSTDLSDSKCTAGTNTVTFNDGDKDISIDVFEKSTVDP 180
Db 121 DTKAIGTTLTLPFSGVSGSDVLANSCQCTAGTNTVTFNDGTSISTVDFEKTVAS 180
Qy 181 SAYLYASRVMSLKNKVTTLFVAPQCENGYTSCTGTFSSNGDVDAIDCSNHIHIGTKGLND 240
Db 181 SDRLLSRILPSLQANLFLPQECANGYTSCTGTFAGTAGCATIDCSNVHIGSGLND 240
Qy 241 WNPVSSSESYTKTCTNSGQIKYQNVPAQYRPFIDAYISATDVNQYTLAYTNDYTCAG 300
Db 241 WNPVSSSESYTKTCTNSGQIKYQNVPAQYRPFIDAYISATDVNQYTLAYTNDYTCAG 300
Qy 301 SRLQSKPTLRTWYTKNSDAGSNGIVIVATRTVTDSTTAVTTLFPNPSVDKTKTIELQ 360
Db 301 AASVDDSFTHWGRYSNQSANGITIVVTRTVDSTTAVTTLFPNPSVDKTKTIELQ 360
Qy 361 PIPTTTITTSYGVVTSYLTAPIGETATVIVDVPHHTTTTWTSEWGTGTTTTTTRNP 420
Db 361 PIPTTTITTSYGVVTSYLTAPIGETATVIVDVPHHTTTTWTSEWGTGTTTTTTRNP 420
Qy 421 TDSIDTVVQVPLNPVTSTTEYWSQSFATTTTVPAGGTDVLIIEP 469
Db 421 TDSIDTVVQVPLNPVTSTTEYWSQSFATTTTVPAGGTDVLIIEP 469

RESULT 9
US-10-245-802-24
; Sequence 24, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
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; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-245-802-24

Query Match      26.4%; Score 1717.5; DB 14; Length 468;
Best Local Similarity 68.7%; Pred. No. 2.8e-80;
Matches 322; Conservative 69; Mismatches 77; Indels 1; Gaps 1;

Qy 1 MLOQFTLLFLYLISAKTIITGVDFNSLTSNAANYAFKPGYPTWNAVLSLGDTS 60
Db 1 MLPQFILLFISLTAVSTAKTIITGVDFNSLTSNAANYAFKPGYPTWNAVLSLSTT 60
Qy 61 ANPGDTFTLNMPCVKYTTTSOTSDLTADGVKATCQFYSGERTFTSLTCTVNDALKS 120
Db 61 ADPGDTFTLLPCVFKPFTTQTSVDLTADGVSTATCDFNAGEEFTTFSSLSCTVNSVSVS 120
Qy 121 SIKAFGTTLPIAFNVGGTGSSTDLSDSKCTAGTNTVTFNDGDKDISIDVFEKSTVDP 180
Db 121 YARVSGTVKLPITFNVGGTGSSTDLSDSKCTAGTNTVTFMDGDKTISTTVDPDASVPSP 180
Qy 181 SAYLYASRVMSLKNKVTTLFVAPQCENGYTSCTGTFSSNGDVDAIDCSNHIHIGTKGLND 240
Db 181 SGVITSSRIIPSLKSLFVWPQCENGYTSCTGTFSSNG-ATIDCSNVNIGISKGLND 239
Qy 241 WNPVSSSESYTKTCTNSGQIKYQNVPAQYRPFIDAYISATDVNQYTLAYTNDYTCAG 300
Db 240 YNPVSSSESYTKTCTNSGQIKYQNVPAQYRPFIDAYISATDVNQYTLAYTNDYTCEN 299
Qy 301 SRLQSKPTLRTWYTKNSDAGSNGIVIVATRTVTDSTTAVTTLFPNPSVDKTKTIELQ 360
Db 300 GNTVDPFTLYTYGYKNSEADSGDVIWVTRTVDSTTAVTTLFPNPSVDKTKTIELQ 359
Qy 361 PIPTTTITTSYGVVTSYLTAPIGETATVIVDVPHHTTTTWTSEWGTGTTTTTTRNP 420
Db 360 PIPTTTITTSYGVVTSYLTAPIGETATVIVDVPHHTTTTWTSEWGTGTTTTTTRNP 419
Qy 421 TDSIDTVVQVPLNPVTSTTEYWSQSFATTTTVPAGGTDVLIIEP 469
Db 420 TGSIDTVIVQIPSPDPTTTTTEYFSFASFTTTTITNPPDGTNSVLIIEP 468

RESULT 10
US-09-801-368-104
; Sequence 104, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
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QY 2 LQOFTLLFLYLISASAKT-----ITGVDFSF-----NSLTWSNAANYAP----- 40
Db 10 LAVFTLLAL--TSVASGATEACLPAGQRKSGMNFYQYSLKDSSTYNAAYMAYGYASKT 68
QY 41 -----KPGGYPTW-----NAVLGWSLD--G 58
Db 69 KLGSVGGQTDISIDYNIPCVSSSGTFPCQBDSDYGNMGCKMGACNSQGIAYWSTDLFG 128
QY 59 TSANPGDPTFLNM-----PCVKYITTSQ-----TSVD 85
Db 129 FYTTFTNV--TLEMTGYFLPQTGYTFKFAVDSDAILSVEGATAFNCCAQOQPPISTN 187
QY 86 LTADGVK-----YATQFYSGBEFTTFLCTVDALKSSIKAFGT-----VTLP 131
Db 188 FTIDGKPMWGSGLPNIIEGVYMYAGYIPM-----KVVSNAVSWGLTLPISVTL 238
QY 132 IAFNVGGTSDLEDKSCFTAGTNTVTFNDGDKDISIDVEFEKSTV--DPSAYLYASRMV 190
Db 239 -----DGTVSDDFEG-----YVVSFDD-----DLSQSNCTVPDPSNYA--VSTTT 277
QY 191 PSLNKKVTLFVAPCENGNTSGTNGFSSNGDVAIDCSNIHIGITKGLNDWYVPSSEF 250
Db 278 TTTEPWTGTFSTSTSTEMTTVGTNGVPTDETIVIVIRPTTASTIITTEPMNSTFTST 337
QY 251 SYTKTCTSGIQIKQVNPAGYRPFIDAYISATDVNQVTLAYNDYTCAGSLQSKPPTL 310
Db 338 ELTIVGTNGVKTDETI-----VIRPTTATTAITTEPWNFTFTSTTEL----- 384
QY 311 RWTGYKSDAGSNGI-----VIVATRTVTDSTTAVTTL--PFPNSVDKTKT----- 355
Db 385 -----ITVGTNGLPDDETIIVIRPTTATTAITTTQPNWDTFTSTSTELTTVGTNGL 438
QY 356 -----IBILOPIPTTIIT-----SYGVGTSYLYKTA-----PGETATVIVDPYH 398
Db 439 PTDETIIVIRPTTATTAMTTQPNWDTFTSTSTELTTVGTNGLPTDET--IIVIRPTT 497
QY 399 TTT--TWTSEWGTIT-----TTTTRN--PTSDIVVVOVPLNPPTVSTT-----EY 443
Db 498 ATTAMTTTQPNWDTFTSTSTELTTVGTNGLPTD--ETIIIV-----IRPTTATTAMTTQ 552
QY 444 WSQSFAIT-----TIVTAPPG--GTD--TVIIREPPNHT--VTTTEYWSQSFAIT-----TTV 490
Db 553 WNDFTSTSTEMTTVGTNGLPTDETIIVIRPTTATTAITTEPWNFTFTSTSTEMTV 612
QY 491 TAPPG--GTDs--VIREPPNHT--VTTTEYWSQSFAIT-----TIVTAPPG--GTDs--VII 538
Db 613 TGTNGLPTDETIIVIRPTTATTATTTQPNWDTFTSTSTEMTTVGTNGLPTDETIIV 672
QY 539 REPPNHT--VTTTEYWSQSFAIT-----TIVTAPPG--GTDs--VIREPPNHT--VTTTEY 587
Db 673 RTPPTATTAMTTQPNWDTFTSTSTELTTVGTNGLPTDETIIVIRPTTATTAMTTQ 732
QY 588 WSQSFAIT-----TIVTAPPG--GTD--TVIIREPPNHTV--TTEYWSQSFAIT-----TTV 634
Db 733 WNDFTSTSTEMTTVGTNGLPTDETIIVIRPTTSEGLISITTEPWTGTFSTSTEMTV 792
QY 635 T-----GPPSGDPTVIREPPNHT--VTTTEYWSQSFAIT-----TITAP-----PGETDVTVI 682
Db 793 TGTNGLPTDETIIVIRPTTSEGLVTTTTEPWTGTFSTSTEMTITGTNGVPTDETIIV 852
QY 683 REPPNHTV--TTEYWSQSFAIT-----TIVTAPPG--GTD--TVIIREPPNHTV--TTEY 731
Db 853 RTPPTSEGLISITTEPWTGTFSTSTEMTITGTNGVPTDETIIVIRPTTSEGLISITTE 912
QY 732 WSQSFAITTTVAPPGTD-----TVIIREPPNHTV--TTEYWSQSFAITTTTIVTAPP 782
Db 913 WTGTFSTSTEMTTHVGTNGLPTDETIIVIRPTTSEGLISITTEPWTGTFSTSTEMTV 972
QY 783 GGT-----DVTIYESMSSSKI-----STSNDSITSIIPFSRP----- 816
Db 973 TGTNGVPTDETIIVIRPTTSEGLISITTEPWTGTFSTSTEMTITGTNGVPTDETIIV 1032

QY 817 -----HYNSTTSD--LSTFESSMNTPTSIISDGMLLSLSTTLVTSETT-----TELICS 865
Db 1033 RTPTSEGLVTTTTEPWTGTFSTSTEMTIVGTNGLPTDETIIVIRPTTATTAISLSSSSS 1092
QY 866 DGKECRLSSSGIIVNTP--DSNESSIVTSTVPTASTMTSDSLSDGISATSDNVKSG 923
Db 1093 SQGITSITSSRRPIIT--PFYPSNGTVISSSVISSSVTSLSLFTSSPVISSSVISSTTTS 1151
QY 924 VSVTTSVTVTIQTTPNPLSSSVTSLTQLSSIPSVSESESKVTFTNGDNQSGTHDSQST 983
Db 1152 TSIFSESSKSSV--IPTSSSTSGSESETSSAGSVSS-----SFISSESSKSPYSSSS-- 1204
QY 984 STBIRIVTST-----KVLPPVVSNTDLTSEPTWTRREOPTTLSTTS-----NSITE 1031
Db 1205 ---LPLVTSATTSEATSLPPATT-----TKTSEQTLVTVTSCSHVCTESISP 1252
QY 1032 DIYTSQPTGNGDNTSTN--PVPVTATSLASBEDNKGSGHESASTSLKPSMGNSG 1089
Db 1253 AIYSTATVTVSGVTTTETWCPISITTEKTKGTTEQTETTKQTIVTVTSSCESDVCS 1312
QY 1090 LTTSTREIATTTGPTTEAPSPAVSSGTDVTTPEPTDTRQPTTLST-----SKTNSLV 1142
Db 1313 KTASPAIVSTSTATINGVTTTWCPIST--TESRQQTTLVTVTSCSGVCSSETASPAI 1370
QY 1143 ATT-----QATNNGGKSPSTDLTSSLTGT--SATSANSELVTSQSV 1184
Db 1371 VSTATATVNDVTVPTWTRPQTANESVSSKMSATGETTTNTLAETTTNTVAETITN 1430
QY 1185 TGA-----VASASNDQSHSTV-----TNSNSIVNTPTOTTLSSQ 1220
Db 1431 TGAETKTVVTSLSRSHATQASATDVIGHSSSVSVSETGNTKSLTSSGLSTMSQ 1490
QY 1221 VTSSP-----STNTPIASTYDGSIIQHSWLYGLITLLSLFI 1260
Db 1491 PRSTPASSVGVYSTASLEISTYAGSANSLLAGSLSVFIASLLAL 1536

RESULT 12

US-10-324-035-17

Sequence 17, Application US/10324035

Publication No. US20050084848A1

GENERAL INFORMATION:

APPLICANT: Phillips, John

TITLE OF INVENTION: METHODS OF USING GLUCAN SYNTHASE PATHWAY REPORTER GENES TO SCREEN

FILE REFERENCE: 9301-178-999

CURRENT APPLICATION NUMBER: US/10/324,035

CURRENT FILING DATE: 2002-12-19

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn version 3.0

SEQ ID NO 17

LENGTH: 1537

TYPE: PR1

ORGANISM: Saccharomyces cerevisiae

US-10-324-035-17

Query Match

Best Local Similarity 14.5%; Score 939; DB 17; Length 1537;

Matches 414; Conservative 246; Mismatches 520; Indels 426; Gaps 84;

QY 2 LQOFTLLFLYLISASAKT-----ITGVDFSF-----NSLTWSNAANYAP----- 40
Db 10 LAVFTLLAL--TSVASGATEACLPAGQRKSGMNFYQYSLKDSSTYNAAYMAYGYASKT 68
QY 41 -----KPGGYPTW-----NAVLGWSLD--G 58
Db 69 KLGSVGGQTDISIDYNIPCVSSSGTFPCQBDSDYGNMGCKMGACNSQGIAYWSTDLFG 128
QY 59 TSANPGDPTFLNM-----PCVKYITTSQ-----TSVD 85
Db 129 FYTTFTNV--TLEMTGYFLPQTGYTFKFAVDSDAILSVEGATAFNCCAQOQPPISTN 187
QY 86 LTADGVK-----YATQFYSGBEFTTFLCTVDALKSSIKAFGT-----VTLP 131

Db 188 FTIDGKPMGSLPPNIEGTVMYAGYYIPM-----KVYVNAVSGTLPISTVLP 238
Qy 132 IAFVNGGTGSTDLEDSKCTAGTNTVTFNDGDKDISIDVEPEKSTV-DPSAYLYASRV 190
Db 239 -----DGTTVSDDFEG-----YVSPFD-----DLQSNCTVPDPNSYA-VSTTT 277
Qy 191 PSLNKKVTLFVAPOCENGYSCTMGFSSNGDVAIDCSNIHIGITKGLDWNTPVSSSEF 250
Db 278 TTTEPWTGTFSTSTEMTGTGNGVPTDETVIVIRPTTASVLIITTEPWNSTFTST 337
Qy 251 SYTKCTSNIGIQKYNVAGYRPFIDAYISATDVNQYTLAYNDVTCAGSRQSKPFTL 310
Db 338 ELITVTGTNGVRVDETI-----VIRPTTATTAITTEPWNSTFTSTSTEL----- 384
Qy 311 RWTGKNSDAGSNGI-----VIVATRTVTDSTTAVTL- PENPSVDKTKT----- 355
Db 385 -----TTVTGTNGLPTDETIIVIRPTTATTATTTQPNWDTFTSTSTELTTVTGTNGL 438
Qy 356 -----TEILOPIPTTIT-----SYVGVTTSYLTKTA-----PIGETATVIVDPVH 398
Db 439 PTDETIIVIRPTTATTATTTQPNWDTFTSTSTELTTVTGTNGLPDET-IIVIRPTT 497
Qy 399 TTT-TVTSEWGTIT-----TTTTN-PTDSIDTVVQVPLNPVTSTT-----EY 443
Db 498 ATTAMTTQPNWDTFTSTSTELITVTGTNGLPTD--ETIIV--IRPTTATTAMTTQP 552
Qy 444 WSQSFAAT-----TTVTAPPG-GTD--TVIIREPNHT--VTTEYMSQSFAAT-----TTV 490
Db 553 WNDFTSTSTEMTGTGNGLPTDETIIVIRPTTATTATTTTEPWNSTFTSTSTEMT 612
Qy 491 TAPPG-GTDS--VLIIREPPNPT--VTTEYMSQSFAAT-----TTVTAPPG-GTDS--VII 538
Db 613 TGNGLPTDETIIVIRPTTATTATTTQPNWDTFTSTSTEMTGTGNGLPTDETIIV 672
Qy 539 REPPNPT--VTTEYMSQSFAAT-----TTVTAPPG-GTDS--VLIIREPPNHT--VTTEY 587
Db 673 RTPTTATTAMTTQPNWDTFTSTSTELITVTGTNGLPTDETIIVIRPTTATTAMTTQP 732
Qy 588 WSQSFAAT-----TTVTAPPG-GTD--TVIIREPNHT--VTTEYMSQSFAAT-----TTV 634
Db 733 WNDFTSTSTEMTGTGNGVPTDETVIVIRPTSEGLISTTTEPWTGTFTSTSTEMT 792
Qy 635 T---GPSGDTVLIIREPPNPT--TVIITTEYMSQSFAAT-----TTITAP-----PGEDTVLI 682
Db 793 TGNGQPTDETVIVIRPTSEGLISTTTEPWTGTFTSTSTEMTGTGNGVPTDETVI 852
Qy 683 REPPNHTV--TTTEYMSQSFAAT-----TTVTAPPG--TD--TVIIREPPNHTV--TTTEY 731
Db 853 RTPTSEGLISTTTEPWTGTFTSTSTEMTGTGNGQPTDETVIVIRPTSEGLISTTTEP 912
Qy 732 WSQSFAATTTVTAPPGGTD-----TVIIREPNHTV--VTTEYMSQSFAATTTVTAPP 782
Db 913 WTGFTSTSTEMTGTGNGVPTDETVIVIRPTSEGLISTTTEPWTGTFTSTSTEMT 972
Qy 783 GGT-----DTVIIYESMSSSKI-----STSSNDITSIIPSFRP----- 816
Db 973 TGNGQPTDETVIVIRPTSEGLISTTTEPWTGTFTSTSTEMTGTGNGQPTDETVI 1032
Qy 817 -----HYVNSTGSD-LSTFESSMNTPTSISSDGLLSSTLVSEIT-----TELICS 865
Db 1033 RTPTSEGLIVTTTTEPWTGTFTSTSTEMTGTGNGLPTDETVIVIRPTTAISSSSSS 1092
Qy 866 DGKCSRLLSSSGVITNP--DSNESSIVTSTVPTASTMSDLSSTDCISATSSDNVSKSG 923
Db 1093 SQQTSSITSRPIIT-PFPYNSGTSVISSSVISSVSSVSSLTSSPVISSSVISSSTTS 1151
Qy 924 VSVTTERSVTTIOTPNPLSSSVTLQLQSLIPSVSESKVPTFSGNDQSGTHDSQST 983
Db 1152 TSIFSESSKSV--IPTSSSTSGSSESTSSAGSVSS-----SPISSESSKSPYSSSS- 1204
Qy 984 STEIEIVTST-----KVLPPVSSNDLTSEPTNTREQPTLSTTS-----NSITE 1031
Db 1205 ---LPLVTSTSTOETASSLPAT-----TKTSEQTLTVTVTSCSHVCTESIP 1252

Qy 1032 DITTSOPTGNDGNTSSN--EVPVATATSLASEDNKSGSHESASTSLKPSMGENSG 1089
Db 1253 AIVSTATVTVSGVTEYITWCPISITEITTKQKGTTEQTTKQTVTVTSSCESDVCS 1312
Qy 1090 LTTSTEIEATTSPTPEAPSPVSSGTDVTTTEPTDTRREQPTLSTT-----SKTNSELV 1142
Db 1313 KTASPAIVSTATINGVTTEYITWCPIST--TESRQQTLLVTVTSCSGVCSSETASPAI 1370
Qy 1143 ATT-----QATNENGKSPSDTLTSSLTCT--SASTSANGSELVTSGSV 1184
Db 1371 VSTATATVNDVVTVTPWRPOTANESVSSKNSATGETTTNLAAETTTVAETIYN 1430
Qy 1185 TCGA-----VASANDQSHSTSV-----TNSNSIVSNTPQTTLSSQ 1220
Db 1431 TGAETKTVVTSLSRSNHAETQATASATDVIGHSSSVSVSETGNTKSLTSSGLSTMSQ 1490
Qy 1221 VTSSSP-----STNFFIASTYDGGSGIIQHSWTLYGLITLLSLFI 1260
Db 1491 PRSTPASSVMGYSTASLEISTYAGSANSLLAGSLSVFIASLLAI 1536

RESULT 13

US-09-801-368-114
; Sequence 114, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 114
; LENGTH: 1322
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-114

Query Match 14.4%; Score 932.5; DB 9; Length 1322;
Best Local Similarity 28.1%; Pred. No. 1.8e-39;
Matches 400; Conservative 215; Mismatches 468; Indels 339; Gaps 79;
Qy 28 NSLTWNAANYAKPGGYTWNALGWSLDGTSANPGDFTLNMPCVFKYTSQT-----S 83
Db 50 DSSTYNAAYMAY---GYASKT-----KLGSGVGQTDIDIDYNI PCV---SSSGTFFCPQ 98
Qy 84 VDLTAD-GVK-YATCQ-----PYSGEFTTFTCTCTVNDALKSSIKAPGTVTLPIA-- 133
Db 99 EDLYGNWKGKIGACSNPIIAVWSYDNLGFGYTTPT-----NVTLEMTGY 143
Qy 134 FNVGGTSGSTDLSDSKCFTAGTNTVTFNDGDKDISIDVEFEKSTVDPSPAYLYASRVMSPL 193
Db 144 FLPPQTGSYI-----FKPATVDDSAI----- 165
Qy 194 NKVTTFLVAPQCENGYTGTMGFSNGSDVAIDC-----SNIHIGITKGLNDWN- 242

Db 166 -----SVGSIAPFCAQEPPISTNFTI---NGIKPWNG 198
Qy 243 -YPVSSBSFSYTKTCTSGNGIQKQNVPA-GYRPF-----IDAYISATDVN- 286
Db 199 SPPDNITGTVMYAGFYPMKIVSNVAVWGTLFISVTLPGTTVSDDFEGVYVTFNNL 258
Qy 287 ---QYTLAYNDYTCAGSRLOSKPFTLRWGYKNSDA-----GSNGI-----VIVATT 331
Db 259 SQPNCTIPDPSNYTVSTIITTEP-----WTGFTSTSTEMTVTGTNGVPTDEIVIRT 314
Qy 332 RTVDSITAVTTLFNPNSVDKTKIEILQIPPTTIT--TSYGVGTVTSYLTKTAPIGETAT 390
Db 315 PT-TASTIITTEPWNSTFTST------ELTIVTGTNGVPTDEIVIRTPTTATTA 366
Qy 391 VIVDPVHTVTTVTSEMTGTTTTTTRN--PTDSIDTVVQVPLNPT-VSTTEYWSQS 447
Db 367 ITTTEPWNSTFTST----TELTIVTGTNGVPTDE-ITIIVIRTPTTATTAITTPQWNDT 421
Qy 448 PATT-----TTVTAPP-GTD--TVIIRPPNHT--VTTEYWSQSFAIT-----TTVTAPP 494
Db 422 FTSTSTELTIVTGTNGVPTDEITIIVIRPTTATTAMITTPQWNDTFTSTTELTIVIRTGTN 481
Qy 495 G-GTDS--VIIRPPNPT--VTTEYWSQSFAIT-----TTVTAPP-GTDS--VIIRPP 542
Db 482 GLPTDEITIIVIRPTTATTAMITTPQWNDTFTSTTEITVTGTNGVPTDEITIIVIRPT 541
Qy 543 NPT--VTTEYWSQSFAIT-----TTVTAPP-GTDS--VIIRPPNHT--VTTEYWSQS 591
Db 542 TATTAMITTPQWNDTFTSTSTEMTVTGTNGVPTDEITIIVIRPTTATTAMITTPQWNDT 601
Qy 592 YATT-----TTVTAPP-GTD--TVIIRPPNHT--VTTEYWSQSFAIT-----TTVTGP- 637
Db 602 FTSTSTEMTVTGTNGVPTDEITIIVIRPTTATTAMITTPQWNDTFTSTSTEMTVTGTN 661
Qy 638 --PSGTDTVIIRPPNPT--VTTEYWSQSFAIT-----TTITAP-----PGETDVTVLIRPP 686
Db 662 GLPTDEITIIVIRPTTATTAMITTPQWNDTFTSTTEITVTGTNGVPTDEITIIVIRPT 721
Qy 687 NPT--VTTEYWSQSFAIT-----TTVTAP-----PGETDVTVLIRPPNHTV--VTTEYWSQS 735
Db 722 TATTAMITTPQWNDTFTSTSTEMTVTGTNGVPTDEITIIVIRPTSEGLISTTEPWTGT 781
Qy 736 YATT-----TTVTAPP-GTD--TVIIRPPNPT--VTTEYWSQSFAIT-----TTVTAPP 782
Db 782 FTSTSTEMTVTGTNGVPTDEITIIVIRPTSEGLVTTTEPWTGTFTSTSTEMTVTGTN 841
Qy 783 G-GTDTVIIRESMS--SSKISTSSNDITSIIPS---FSRPHYVNSTTSDLTFFESSM 834
Db 842 QOQDTEVIIKPTAISLSSLSGGQITSPITSARPIITFPYPSNGTSVSSSVISS 901
Qy 835 NPTPTSISSDGM---LLSSTLVTESETTEILICSGKCSRLLSSSGIVTAPDNESSIV 891
Db 902 DTSSLVSSSVTSLVTSPPVSSSFISPVSSSTTSASILSESS-----K 948
Qy 892 TSVTPTASTMSDLSLSTGIGISATSDNVSKSVSTTSTSVTITOTPNLSSSVTSLQ 951
Db 949 SSVIPTSSSTSGSESESTGASASAS---SSSISSESPKSTVSSSLP-PVTSATTSOEI 1004
Qy 952 LSSIPSVSESKSVFTSGNDNQSGTHDSQSTSTIEIVTSTSTKVLPPVWSSNDLTASE 1011
Db 1005 TSSLPVPVTTKT-----SQOTLVTVTSCESHVCTESISSAIVSTAT 1046
Qy 1012 PT---NTRQOFTLSTGNSITEDIT-TSQPTGNDGNDTSSNPVPTVATSTLASASED 1067
Db 1047 VTVSGATTETVTCPISTTEITKQTEITKQTKGTEQITTEITKQTVVT---ISSCESD 1103
Qy 1068 --NKSGSHESASTSLKPSMGENSEGLTTEITEATTSPEAPSPAVSGTDVTTPTDTR 1125
Db 1104 VCSKTASPAIVSTATINGVTVTTCPISTTESKQOTTLVTVTSCGSGVCSETT--- 1160
Qy 1126 EQPTLSTLSTKNSSELVAT-----TQATWNGKSPSDDLSTSLTGTSTASAT-----SA 1174

Db 1161 -SPAIVSTATATVNDVVTVSTWRPOTTNEQSVSSKMSNSATSETTNTGAAETTTSTGAA 1219
Qy 1175 NSBLVTSGSVT-----GGAVASASNDQSHSTSV-----TMSNSIVSNPTQTLSSQQTSS 1224
Db 1220 ETKTVTVTSISRFNHAETQATSDTVIGHSSVVSVSETGNTKSLTSSGLSTMSQQRST 1279
Qy 1225 -----SPSTNTFIATDQSGSIIQHSHTWLYGLITLLSLFI 1260
Db 1280 PASSMWGSSSTASLEISTYAGSANSLLAGSLGVFIASLLALAI 1321
RESULT 14
US-10-369-493-1353
; Sequence 1353, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B US/10369,493
; CURRENT APPLICATION NUMBER: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 1353
; LENGTH: 1322
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-1353

Query Match 14.4%; Score 932.5; DB 15; Length 1322;
Best Local Similarity 28.1%; Pred. No. 1.8e-39;
Matches 400; Conservative 215; Mismatches 468; Indels 339; Gaps 79;
Qy 28 NSLTWMSNAANVAPKPGVPTWNAVLGWSLDGTSANPGDTFTLNNPCVFKYTTSTQ-----S 83
Db 50 DSSITSNNAWAY---GYASKT-----KLSGVGGQTDISIDYINPCV---SSSGTFFPCPQ 98
Qy 84 VDLTAD-GVK-YATCQ-----FYSGBEFTFTSLTCTVNDALKSSIKAFOTVTLPIA-- 133
Db 99 EDLYGNWCKGIGACSNPIIAYWSTDLFGYTTPT-----NVTLEMTGY 143
Qy 134 FNVGGTGSSTULEDSKCTAGTNTVTFNDGDKDISIDVEPEKSTVDPASLYASRVMSPL 193
Db 144 FLPPQTGSYT-----FKPATVDDSAI----- 165
Qy 194 NKVTTLFVAPQENGYTSGTMGFSSNGDVAIDC-----SNHIGITKGLNDWN- 242
Db 166 -----SVGSIAPFCAQEPPISTNFTI---NGIKPWNG 198
Qy 243 -YPVSSBSFSYTKTCTSGNGIQKQNVPA-GYRPF-----IDAYISATDVN- 286
Db 199 SPPDNITGTVMYAGFYPMKIVSNVAVWGTLFISVTLPGTTVSDDFEGVYVTFNNL 258
Qy 287 ---QYTLAYNDYTCAGSRLOSKPFTLRWGYKNSDA-----GSNGI-----VIVATT 331
Db 259 SQPNCTIPDPSNYTVSTIITTEP-----WTGFTSTSTEMTVTGTNGVPTDEIVIRT 314
Qy 332 RTVDSITAVTTLFNPNSVDKTKIEILQIPPTTIT--TSYGVGTVTSYLTKTAPIGETAT 390
Db 315 PT-TASTIITTEPWNSTFTST------ELTIVTGTNGVPTDEIVIRTPTTATTA 366
Qy 391 VIVDPVHTVTTVTSEMTGTTTTTTRN--PTDSIDTVVQVPLNPT-VSTTEYWSQS 447
Db 367 ITTTEPWNSTFTST----TELTIVTGTNGVPTDE-ITIIVIRTPTTATTAITTPQWNDT 421
Qy 448 PATT-----TTVTAPP-GTD--TVIIRPPNHT--VTTEYWSQSFAIT-----TTVTAPP 494

Db 422 FTSTSTBLTAVTGTNGLPDDETIIVIRPTATTATTMTTQPMNDTFTSTSTELTIVTGTN 481
Qy 495 G-GTDS--VLIIRPPNPT--VTTTEYWSQSFAIT---TTVTAPPG-GTDS--VLIIRPP 542
Db 482 GLPDTETIIVIRPTTATTATTMTTQPMNDTFTSTSTELTIVTGTNGLPDDETIIVIRPT 541
Qy 543 NPT--VTTTEYWSQSFAIT---TTVTAPPG-GTDS--VLIIRPPNPT--VTTTEYWSQS 591
Db 542 TATTAMTTQPMNDTFTSTSTEMTTVGTNGLPDDETIIVIRPTTATTATTMTTQPMNST 601
Qy 592 YATT---TTVTAPPG-GTD--VLIIRPPNPT--VTTTEYWSQSFAIT---TTVTGP- 637
Db 602 FTSTSTEMTTVGTNGLPDDETIIVIRPTTATTATTMTTQPMNDTFTSTSTEMTTVGTN 661
Qy 638 --PSGTDVLIIRPPNPT--VTTTEYWSQSFAIT---TTVTAP--PGETDVLIREPP 686
Db 662 GLPDTETIIVIRPTTATTATTMTTQPMNDTFTSTSTELTIVTGTNGLPDDETIIVIRPT 721
Qy 687 NHT--VTTTEYWSQSFAIT---TTVTAP---PGETDVLIREPPNHTV--VTTTEYWSQS 735
Db 722 TATTAMTTQPMNDTFTSTSTEMTTVGTNGVPDDETIIVIRPTSEGLISITTEPWGT 781
Qy 736 YATT---TTVTAPPG-GTD--VLIIRPPNPT--VTTTEYWSQSFAIT---TTVTAPP 782
Db 782 FTSTSTEMTTVGTNGQPDDETIIVIRPTSEGLVTTTTEPWGTFTSTSTEMTTITGTN 841
Qy 783 G--GTDVLIIRPPNPT--SSKISTSSNDITSLIPS---PSRPHVNSVTSDLSTPSSSM 834
Db 842 GQPDDETIIVIRPTTATTATTMTTQPMNDTFTSTSTEMTTVGTNGVPDDETIIVIRPT 901
Qy 835 NPTSTSSDCM---LLSSTLVASETTTTELICSDGKCEKSRSSSGSIVTNPDSNESSIV 891
Db 902 DTSSLVSSSVTSLSVTSPISSPFISSPVISSVTSSTTASILSESS-----K 948
Qy 892 TSVPTASTMDSLSSTPDGTSATSSONVSGSVVTEVTSVTTIQTTPNPLSSSVTSLTQ 951
Db 949 SSVIPTSSTSGSESESTGASASAS---SSSSISSESPKSTYSSSLIP-PVTSATTSQEI 1004
Qy 952 LSSIPSVSESKVFTTNSGDNQSGHDSQSTSTELTIVTSSTKVLPPVVSNTDLTSE 1011
Db 1005 TSSLPPVTTTKT-----SEQTLLVTVTSCHSVCTESISSAIVSTAT 1046
Qy 1012 PT---NREQPTLSTTSNITEDIT-TSQPTGDNQNTSSINPVPVATSTLASASEED 1067
Db 1047 VTVSGATETVTCPISTETITKQTTETTKQTKTEQTTETTKQTTVVT---ISSCED 1103
Qy 1068 --NKGSHGESASTLKPMSGENGLTSTIEIATTSPTAPSPAVSSGDDVTEPTDTR 1125
Db 1104 VCSKTASPAIVSTSTATINGVTEYTTWCPISTTESKQQTLLVTVTSCHSVCTESSETT--- 1160
Qy 1126 EQPTLSTTKTNSSELVAT---TOATNENGKSPSTDLTSSITGTSAST-----SA 1174
Db 1161 -SPAIVSTATVNDVVTVTSWRPQNTNEQSVSSKNSAISSETTNTGAEATTTSTGAA 1219
Qy 1175 NSELVTSQSVT-----GGAVASASNDQSHSTSV-----TNSNSIVSNTPOTLLSQQVTS 1224
Db 1220 ETKTVTSSISRFNHAEQTASATDVIGHSSVVSVSETGNTKSLSSGLSTWSQPRST 1279
Qy 1225 -----SPSTNTVFIASDYGSGSIHQHSTWLYGLITLLSLFI 1260
Db 1280 PASSMWGSSTASLEISTYAGSANSLLAGSLSVFIASLLALAI 1321

RESULT 15

US-09-922-217-1068
; Sequence 1068, Application US/09922217
; Patent No. US2002007641A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy

; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuxiu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922,217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1068
; LENGTH: 5179
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-922-217-1068

Query Match 11.1%; Score 721.5; DB 9; Length 5179;
Best Local Similarity 25.3%; Pred. No. 6e-28;
Matches 335; Conservative 158; Mismatches 554; Indels 279; Gaps 54;

Qy 59 TSANPGDTEFLNMPGVFKYTTSTQTSVDLPADGKVKATCOFYSGEEFTTSTLTCTVNDAL 118
Db 1647 TTTTPTTTPSPSP-----TTTTPSPPIITTTTTPPPTT-----TPSSPITTTSPPT 1693
Qy 119 KSIIKAFGVTVLPIARNVCGTSSDLESKCTAGTNTVFNDDGDKDISIDVEPKSTV 178
Db 1694 TMTTTPSPPTTTPSPPIITTTTTTTPSSSTTTPSPPTTMTTTPSPPTTMT-----TTL 1747
Qy 179 DP---SAYLYASRVMSLKNVT-----TLFVAPQCE-NGY-TSGTMGFSSSSNGDVA 224
Db 1748 PPTTSSPPTTTPSPPIITPTTTPSPPTTTPTPCPLCNWGLSDGKPNHFKPGDTE 1807
Qy 225 IDCSNIHIGITKGLNDWNPVSSEFSY-----TKTC-TSNGIQIKYQN-VPAGY 272
Db 1808 L-----IGDVGCG-PCGAANISCRATMYPDVPIGQLGQTVCDVSVGLICKNEDQKPGV 1860
Qy 273 RPFIDAYISATDVNQVTLAYNDYTCAGSRLOSKPFLRWTKYKNSDAOSNGIIVATTR 332
Db 1861 IPW-----AFCLNYEINVQCC--ECVTQPTTMTTMTTENPTTPTTPTTPTT 1907
Qy 333 TVTDSFTAVTLLPSPVSKTKTIELQPIPTTITTSYVGVTSYLTCTAPIG-ETATV 391
Db 1908 TPTPTPTGTPT 1967
Qy 392 IVDVPVHTTTTVTSEWGT-----TTTTT-----TRTNPTDSIDTVVVQVP 432
Db 1968 ---TPITTTTPT 2024
Qy 433 LNPPTVSTTEYWSQSFAITTTTAPPGDVTIIRPPNHTVTTTEYWSQSFAITTTTVA 492
Db 2025 TPTPTGTPT 2072
Qy 493 PPGTD-----SVIIRPPNPTVTTTEYWSQSFAITTTTAP-----PGTD-----S 535
Db 2073 TPTGTPT 2132
Qy 536 VIIRPPNPTVTTTEYWSQSFAITTTTAP-----PGTDSVIIRPPNHTVTTTEYWSQS 592
Db 2133 TTTTPT 2180
Qy 593 ATTTTAPPGDVTIIRPPNHTVTTTEYWSQSFAITTTTVPSPGTD-----T 643
Db 2181 -TTVPTPTPTGTPT-----PTTPTPT-----TTVPTPTPTGTPTPTPTPTPTPT 2226
Qy 644 VIIRPPNPTVTTTEYWSQSFAITTTTAPPGDVTIIRPPNHTVTTTEYWSQSFAIT 703
Db 2227 TTVPTPTPTGTPT 2272
Qy 704 TTVTAPPGDVTIIRPPNHTVTTTEYWSQSFAITTTTVPAPGTD-----TVII 754

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